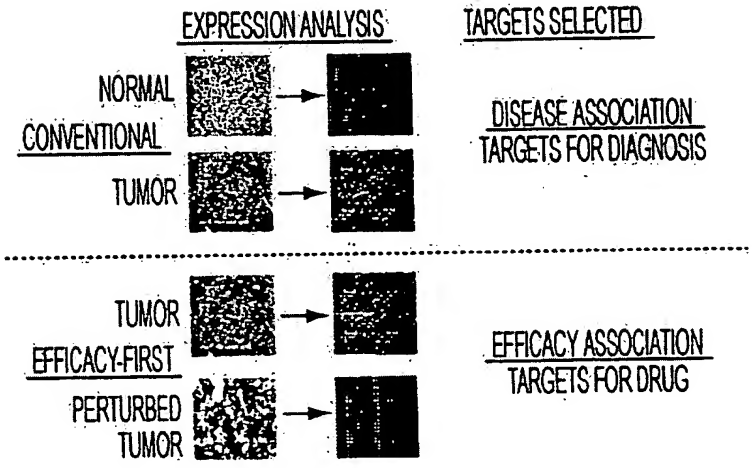
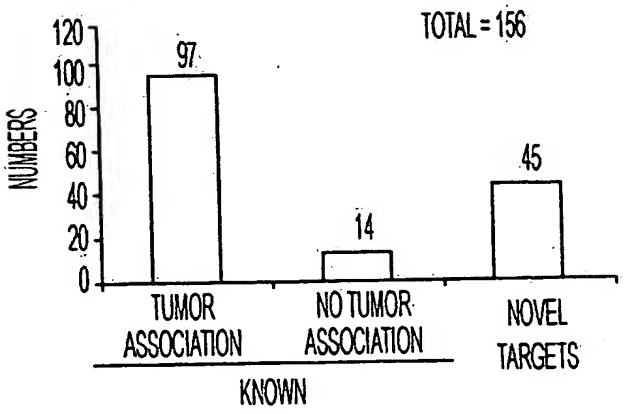
REPLACEMENT SHEET



ADVANTAGE OF EFFICACY-FIRST DISCOVERY™ METHOD

FIG. 1



HIGHLY ENRICHED TUMOR TARGETS

FIG. 2

REPLACEMENT SHEET

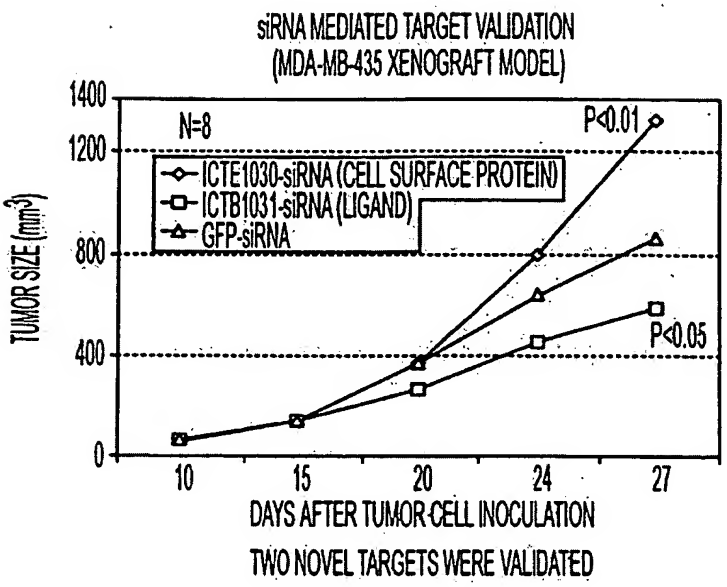


FIG. 3

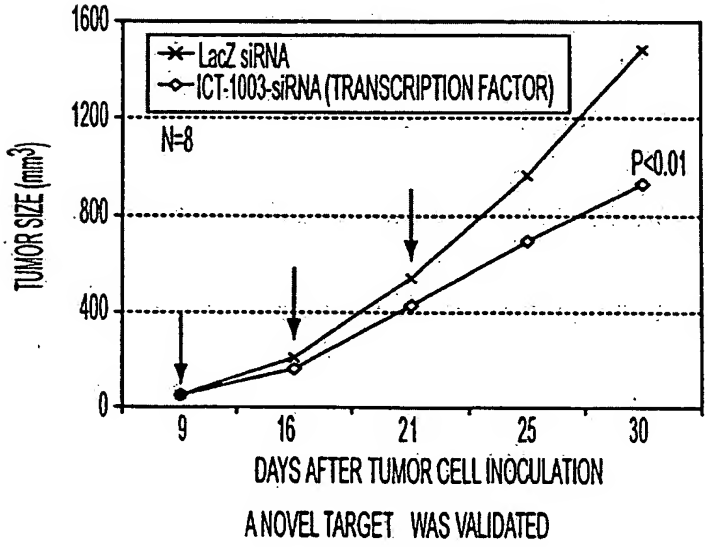


FIG. 4

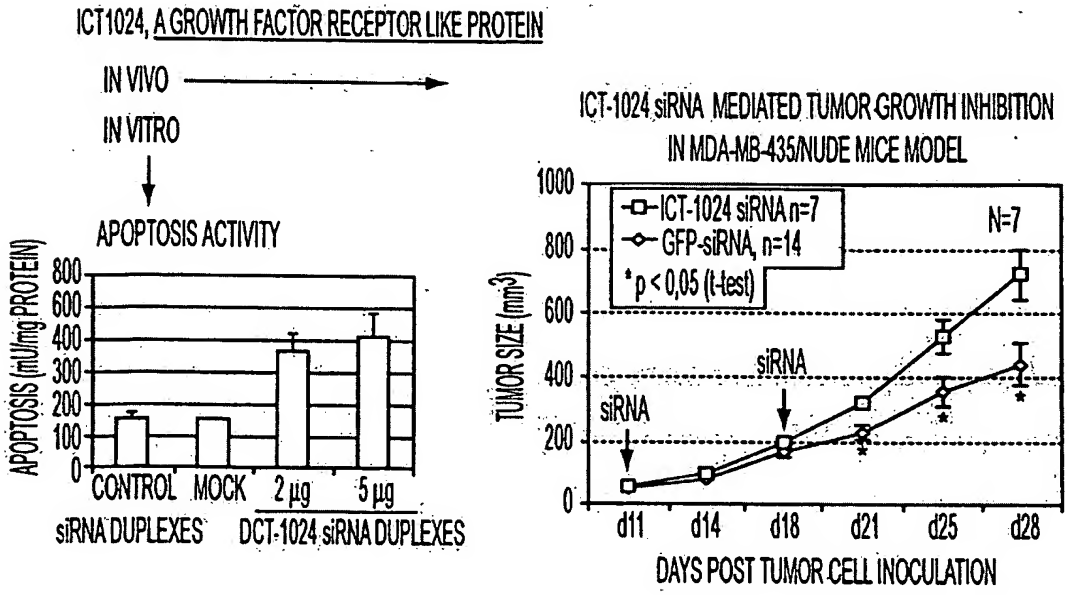

ICT1024, A GROWTH FACTOR RECEPTOR LIKE PROTEIN
IN VIVO
IN VITRO
APOPTOSIS ACTIVITY
APOPTOSIS (mU/mg PROTEIN)
800
600
400
300
200
100
0
CONTROL
MOCK
2 µg
5 µg
siRNA DUPLEXES
DCT-1024 siRNA DUPLEXES
ICT-1024 siRNA MEDIATED TUMOR GROWTH INHIBITION
IN MDA-MB-435/NUDE MICE MODEL
ICT-1024 siRNA n=7
GFP-siRNA, n=14
* p < 0,05 (t-test)
N=7
siRNA
siRNA
TUMOR SIZE (mm3)
1000
800
600
400
200
0
d11
d14
d18
d21
d25
d28
DAYS POST TUMOR CELL INOCULATION

FIG. 5

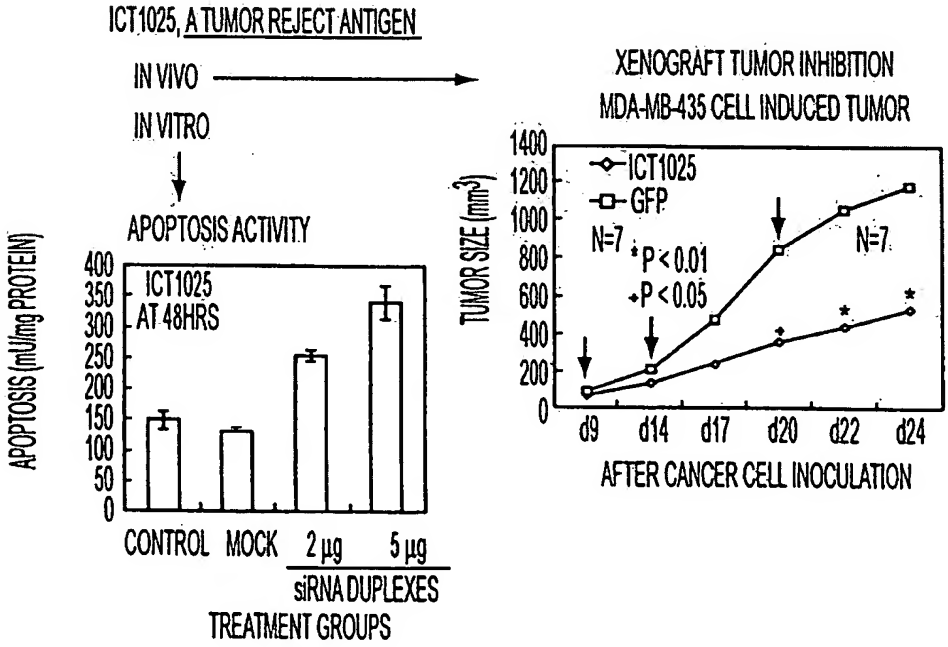

ICT1025, A TUMOR REJECT ANTIGEN
IN VIVO
IN VITRO
APOPTOSIS ACTIVITY
APOPTOSIS (mU/mg PROTEIN)
400
350
300
250
200
150
100
50
0
ICT1025
AT 48HRS
CONTROL
MOCK
2 µg
5 µg
siRNA DUPLEXES
TREATMENT GROUPS
XENOGRAFT TUMOR INHIBITION
MDA-MB-435 CELL INDUCED TUMOR
ICT1025
GFP
N=7
N=7
* P < 0.01
+ P < 0.05
TUMOR SIZE (mm3)
1400
1200
1000
800
600
400
200
0
d9
d14
d17
d20
d22
d24
AFTER CANCER CELL INOCULATION

FIG. 6

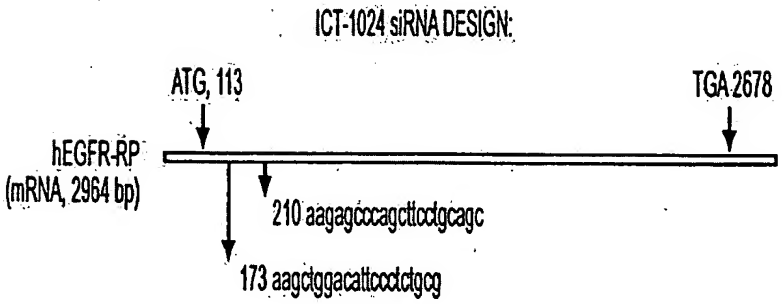

ICT-1024 siRNA DESIGN:
ATG, 113
TGA 2678
hEGFR-RP
(mRNA, 2964 bp)
210 aagagcccagcttcctgcagc
173 aagctggacattcccctgcg

FIG. 7

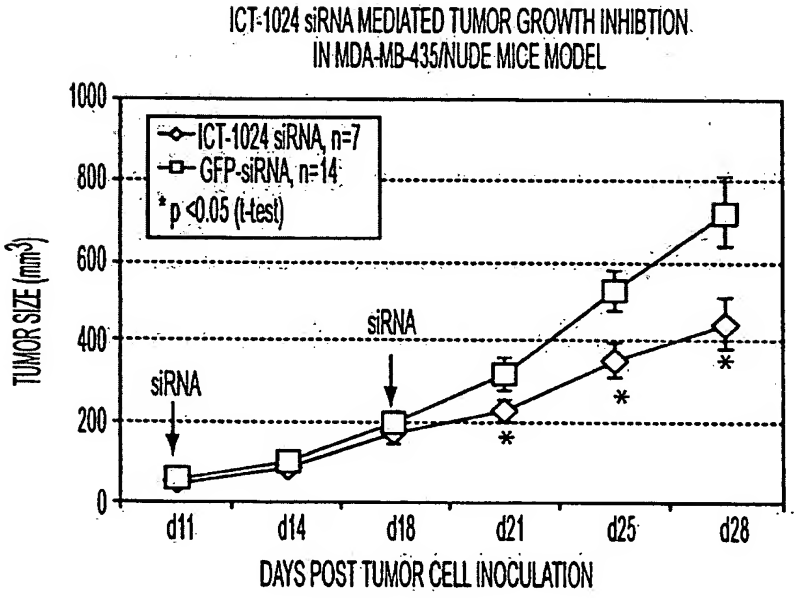

ICT-1024 siRNA MEDIATED TUMOR GROWTH INHIBTION
IN MDA-MB-435/NUDE MICE MODEL
ICT-1024 siRNA, n=7
GFP-siRNA, n=14
* p <0.05 (t-test)
TUMOR SIZE (mm3)
1000
800
600
400
200
0
siRNA
siRNA
d11
d14
d18
d21
d25
d28
DAYS POST TUMOR CELL INOCULATION

FIG. 8

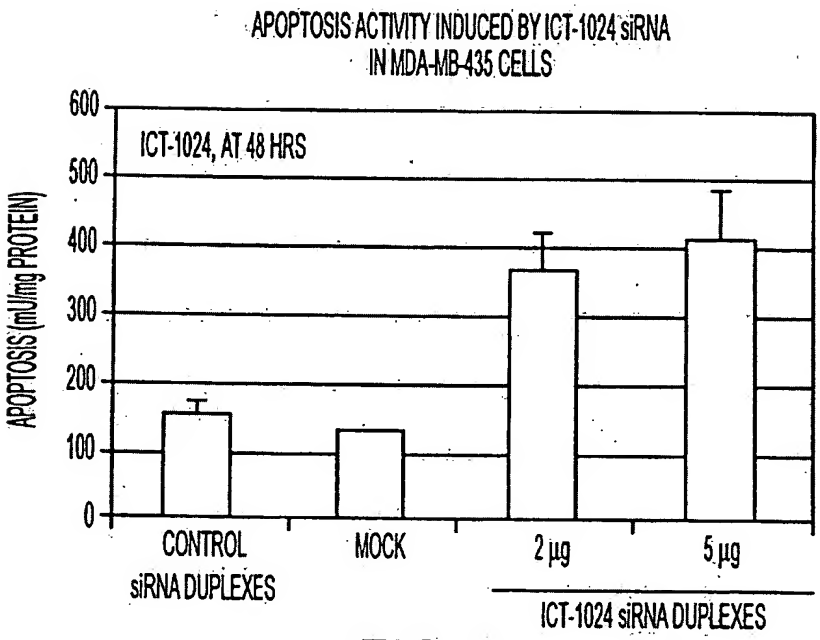

APOPTOSIS ACTIVITY INDUCED BY ICT-1024 siRNA
IN MDA-MB-435 CELLS
ICT-1024, AT 48 HRS
APOPTOSIS (mU/mg PROTEIN)
600
500
400
300
200
100
0
CONTROL
siRNA DUPLEXES
MOCK
2 µg
5 µg
ICT-1024 siRNA DUPLEXES

FIG. 9

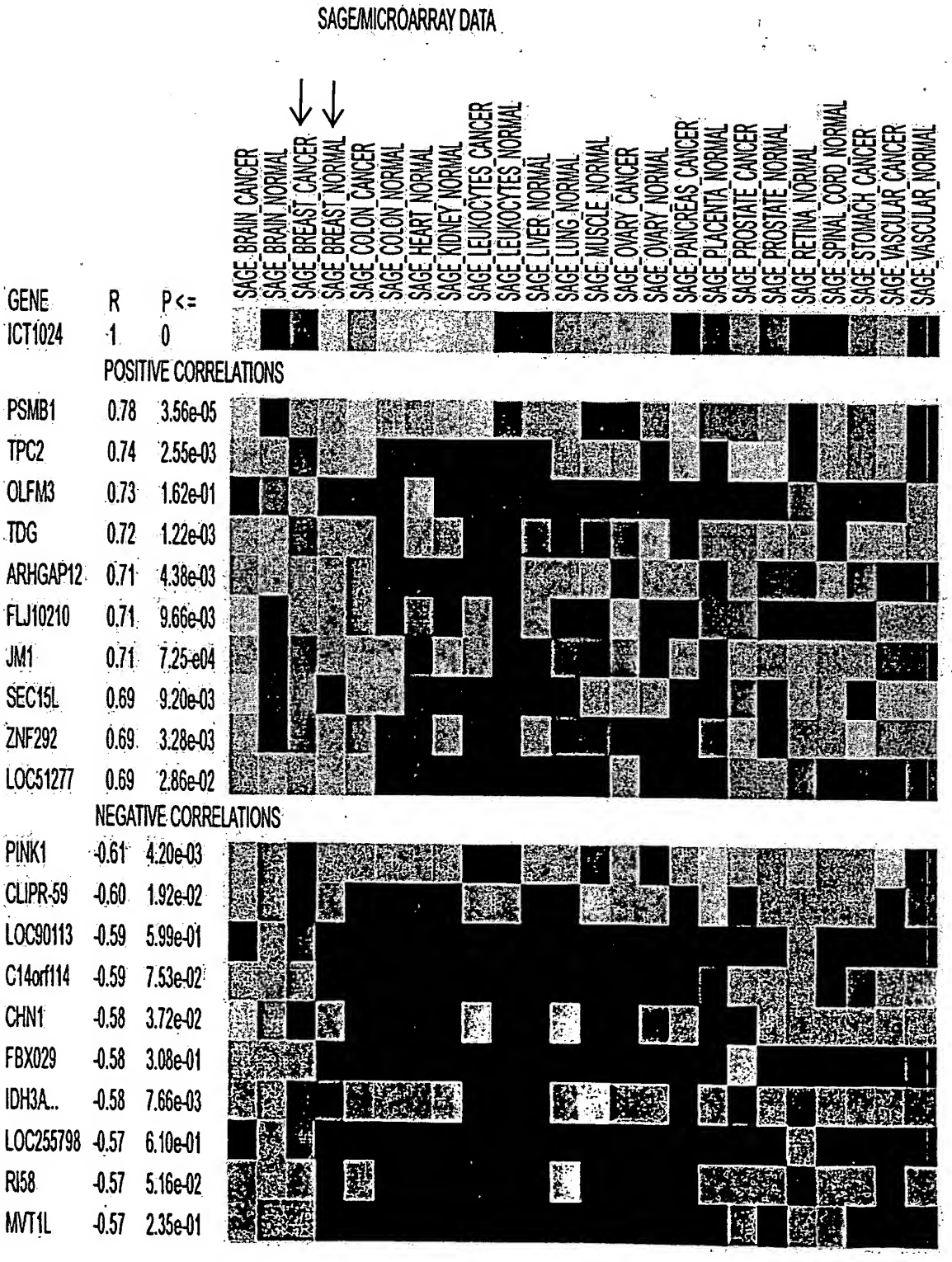

SAGE/MICROARRAY DATA
SAGE_BRAIN_CANCER
SAGE_BRAIN_NORMAL
SAGE_BREAST_CANCER
SAGE_BREAST_NORMAL
SAGE_COLON_CANCER
SAGE_COLON_NORMAL
SAGE_HEART_NORMAL
SAGE_KIDNEY_NORMAL
SAGE_LEUKOCYTES_CANCER
SAGE_LEUKOCYTES_NORMAL
SAGE_LIVER_NORMAL
SAGE_LUNG_NORMAL
SAGE_MUSCLE_NORMAL
SAGE_OVARY_CANCER
SAGE_OVARY_NORMAL
SAGE_PANCREAS_CANCER
SAGE_PLACENTA_NORMAL
SAGE_PROSTATE_CANCER
SAGE_PROSTATE_NORMAL
SAGE_RETINA_NORMAL
SAGE_SPINAL_CORD_NORMAL
SAGE_STOMACH_CANCER
SAGE_VASCULAR_CANCER
SAGE_VASCULAR_NORMAL
GENE R P<=
ICT1024 1 0
POSITIVE CORRELATIONS
PSMB1 0.78 3.56e-05
TPC2 0.74 2.55e-03
OLFM3 0.73 1.62e-01
TDG 0.72 1.22e-03
ARHGAP12 0.71 4.38e-03
FLJ10210 0.71 9.66e-03
JM1 0.71 7.25e-04
SEC15L 0.69 9.20e-03
ZNF292 0.69 3.28e-03
LOC51277 0.69 2.86e-02
NEGATIVE CORRELATIONS
PINK1 -0.61 4.20e-03
CLIPR-59 -0.60 1.92e-02
LOC90113 -0.59 5.99e-01
C14orf114 -0.59 7.53e-02
CHN1 -0.58 3.72e-02
FBX029 -0.58 3.08e-01
IDH3A... -0.58 7.66e-03
LOC255798 -0.57 6.10e-01
RI58 -0.57 5.16e-02
MVT1L -0.57 2.35e-01

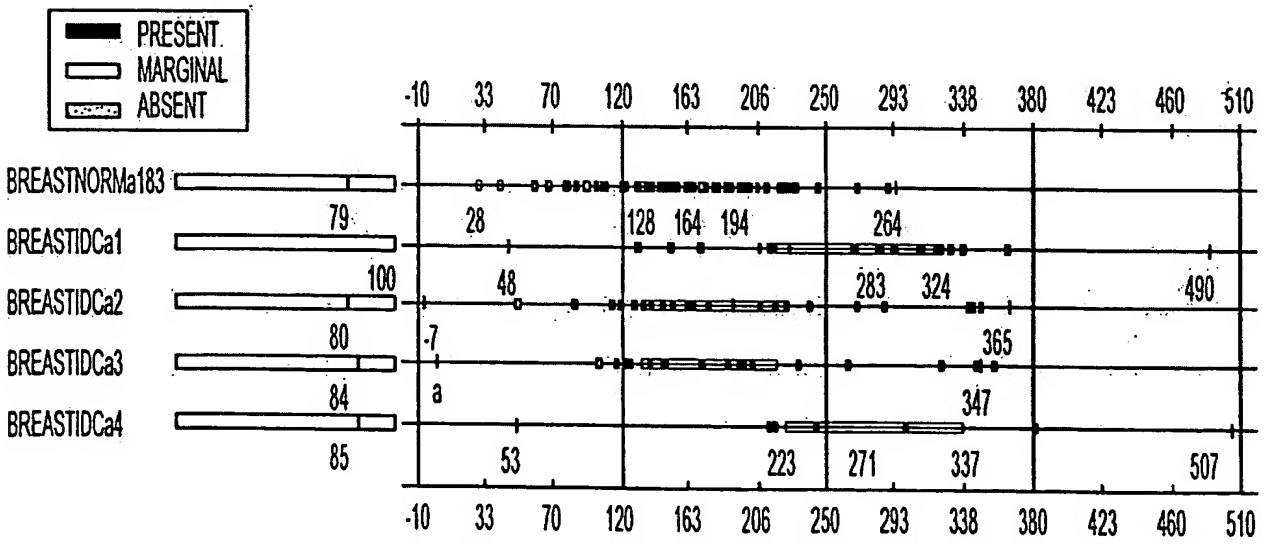
FIG. 10

CANCER TISSUE DISTRIBUTION

FRAGMENT NAME	218686_s_at			
SEQ. ACCESSION	NM_022450			
GENE NAME	LIKELY ORTHOLOG OF MOUSE EPIDERMAL GROWTH FACTOR RECEPTOR; RELATED SEQUENCE			

BREAST NORMAL VS. INFILTRATING DUCT CARCINOMA (IDC) STAGE 1	
FOLD_CHANGE	1.69
DIRECTION	UP
FOLD CHANGE P-VALUE	0

	NORMAL	IDC S-I	IDC S-II	IDC S-III	IDC S-IV
# OF SAMPLES (n)	83	19	30	19	6
MEAN	159.73	264.5	192.96	195.16	284.29
STDDEV	50.03	70.64	82.37	77.41	71.09
MEDIAN	164.53	283.05	191.27	187.7	271.59
PRESENT CAL%	79	100	80	84	83



ICT1024 IS HIGHLY UP REGULATED IN ALL STAGE I BREAST TUMOR SAMPLES (100%)

FIG. 11

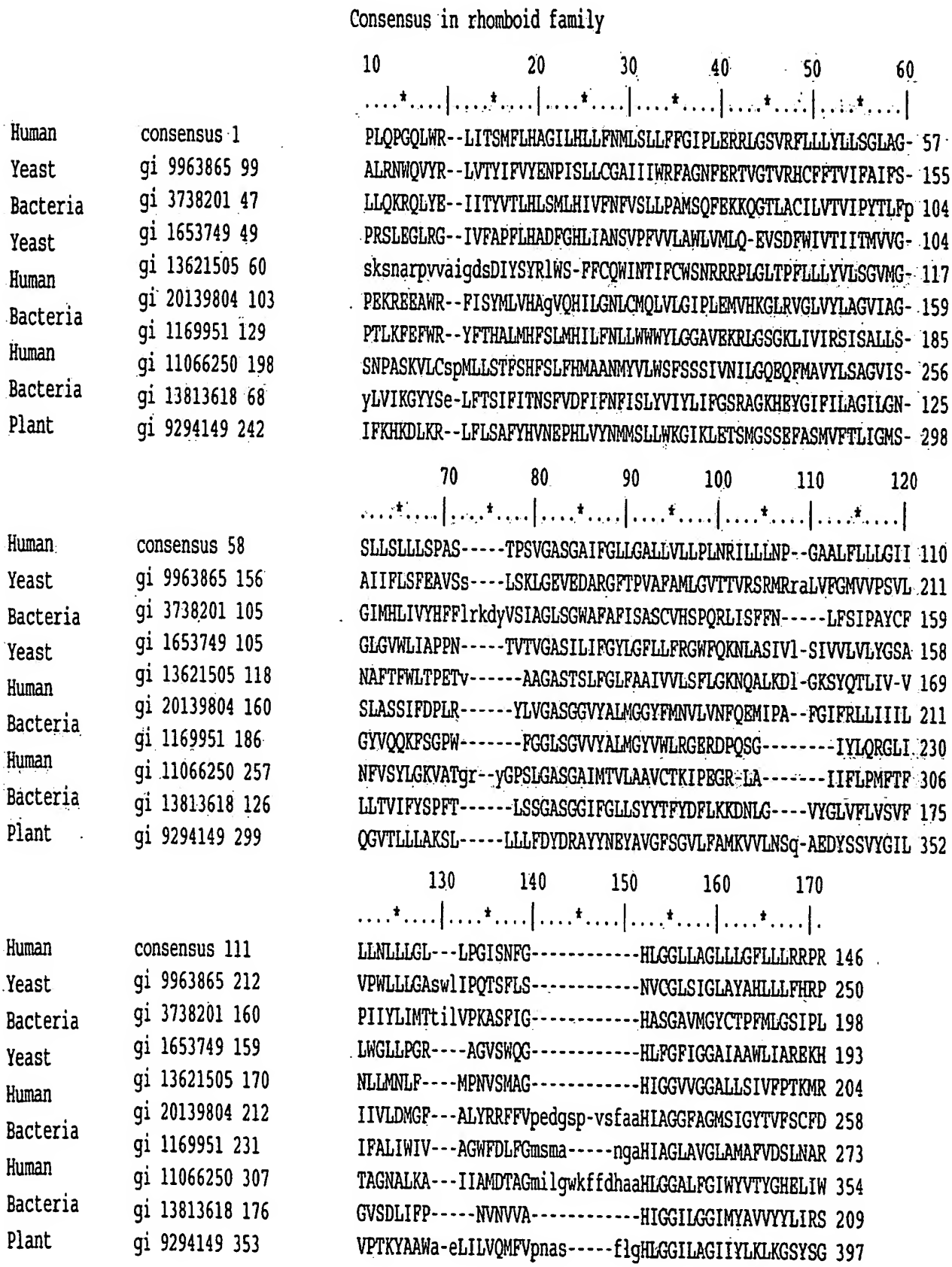

Consensus in rhomboid family
10 20 30 40 50 60
Human consensus 1 PLQPGQLWR--LITSMFLHAGILHLLFNMLSLLFFGIPLERRLGSVRFLLLYLLSGLAG- 57
Yeast gi 9963865 99 ALRNWQVYR--LVTYIFVYENPISLLCGAIIIWRFAGNPERTVGTVRHCFFTVIFAIFS- 155
Bacteria gi 3738201 47 LLQKRQLYE--IITYVTLHLSMLHIVFNFVSLLPAMSQPEKKQGTLACILVTVIPYTLFp 104
Yeast gi 1653749 49 PRSLEGLRG--IVFAPFLHADFGHLIANSVPFVVLAWLVMLQ-EVSDFWIVTIITMVVG- 104
Human gi 13621505 60 sksnarpvvaigdsDIYSYRlWS-FFCQWINTIFCWSNRRRPLGLTPFLLLYVLSGVMG- 117
Bacteria gi 20139804 103 PEKREEAWR--FISYMLVHAgVQHILGNLCMQLVLGIPLEMVHKGLRVGLVYLAGVIAG- 159
Human gi 1169951 129 PTLKFEFWR--YFTHALMHFSLMHILFNLLWWWYLGGAVEKRLGSGKLIVIRSISALLS- 185
Bacteria gi 11066250 198 SNPASKVLCspMLLSTFSHFSLFHMAANMYVLWSFSSSIVNILGQEQFMAVYLSAGVIS- 256
Plant gi 13813618 68 yLVIKGYYSe-LFTSIFITNSFVDFIFNFISLYVIYLIFGSRAGKHEYGIFILAGILGN- 125
gi 9294149 242 IFKHKDLKR--LFLSAFYHVNEPHLVYNMMSLLWKGIKLETSMGSSEFASMVFTLIGMS- 298
70 80 90 100 110 120
Human consensus 58 SLLSLLLSPAS-----TPSVGASGAIFGLLGALLVLLPLNRILLLNP--GAALFLLLGII 110
Yeast gi 9963865 156 AIIFLSFEAVSs----LSKLGEVEDARGFTPVAFAMLGVTTVRSRMRraLVFGMVVPSVL 211
Bacteria gi 3738201 105 GIMHLIVYHFFlrkdyVSIAGLSGWAFAPISASCVHSPQRLISFFN-----LFSIPAYCF 159
Yeast gi 1653749 105 GLGVWLIAPPN-----TVTVGASILIFGYLGFLLFRGWFQKNLASIVl-SIVVLVLYGSA 158
Human gi 13621505 118 NAFTFWLTPETv------AAGASTSLFGLFAAIVVLSFLGKNQALKDl-GKSYQTLIV-V 169
Bacteria gi 20139804 160 SLASSIFDPLR------YLVGASGGVYALMGGYFMNVLVNFQEMIPA--FGIFRLLIIIL 211
Human gi 1169951 186 GYVQQKFSGPW-------FGGLSGVVYALMGYVWLRGERDPQSG--------IYLQRGLI 230
Bacteria gi 11066250 257 NFVSYLGKVATgr--yGPSLGASGAIMTVLAAVCTKIPEGR-LA--------IIFLPMFTF 306
Human gi 13813618 126 LLTVIFYSPFT------LSSGASGGIFGLLSYYTFYDFLKKDNLG----VYGLVFLVSVF 175
Plant gi 9294149 299 QGVTLLLAKSL-----LLLFDYDRAYYNEYAVGFSGVLFAMKVVLNSq-AEDYSSVYGIL 352
130 140 150 160 170
Human consensus 111 LLNLLLGL---LPGISNFG----------HLGGLLAGLLLGFLLLRRPR 146
Yeast gi 9963865 212 VPWLLLGAswlIPQTSFLS----------NVCGLSIGLAYAHLLLFHRP 250
Bacteria gi 3738201 160 PIIYLIMTtilVPKASFIG----------HASGAVMGYCTPFMLGSIPL 198
Yeast gi 1653749 159 LWGLLPGR----AGVSWQG----------HLFGFIGGAIAAWLIAREKH 193
Human gi 13621505 170 NLLMNLF----MPNVSMAG----------HIGGVVGGALLSIVFPTKMR 204
Bacteria gi 20139804 212 IIVLDMGF---ALYRRFFVpedgsp-vsfaaHIAGGFAGMSIGYTVFSCFD 258
Human gi 1169951 231 IFALIWIV---AGWFDLFGmsma-----ngaHIAGLAVGLAMAFVDSLNAR 273
Bacteria gi 11066250 307 TAGNALKA---IIAMDTAGmilgwkffdhaaHLGGALFGIWYVTYGHELIW 354
Human gi 13813618 176 GVSDLIFP-----NVNVVA----------HIGGILGGIMYAVVYYLIRS 209
Plant gi 9294149 353 VPTKYAAWa-eLILVQMFVpnas-----flgHLGGILAGIIYLKLKGSYSG 397

FIG. 12

Human rhomboid Proteins

Human Rhomboid Family Protein Alignments

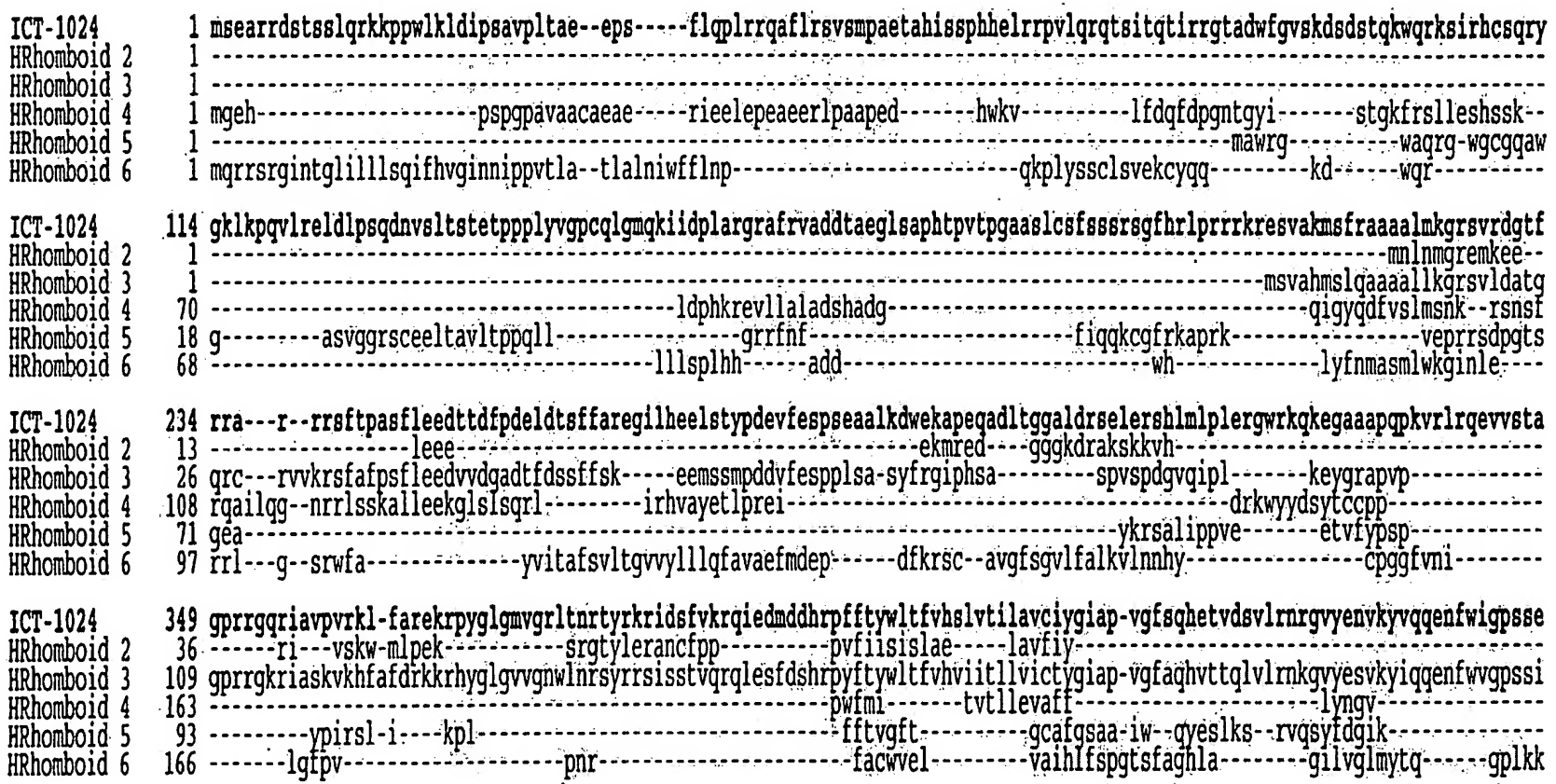


FIG. 13

Applicants: Patrick Y. Lu et al.
Application No.: 10/551,667 Docket No.: INTM/017
Confirmation No.: 5623 Filed: July 18, 2006
For: TARGETS FOR TUMOR GROWTH INHIBITION
Agent: Alla Brukman Reg. No. 61,254 Sheet 9 of 48
Express Mail Label No.: EM125015763US
REPLACEMENT SHEET

```
ICT-1024          467 alihlgakfspcmrqdpqvhsfirsarerekhsaccvrndrsgcvqtseeecsstlavwvkwpihpsap--elaghkrqfgsvchqdprvcdepssedphewpeditkwpictknsagn
HRhomboid 2        78 ------------------------------------------------------------------------yavw------------------------kpqkqw----------
HRhomboid 3       228 dlihlgakfspcirkdqgqieqlvlrerdlerdsgccvqmdhsgciqtqrkdcsetlatfvkwqddtgppmdksdlggkrtsgavchqdprtceepassgahiwpdditkwpicteqarsn
HRhomboid 4       183 ------------------------------------------------------slggfvlgvthpr-------------------------------------------ylknslvy
HRhomboid 5       137 -----adwldsir--pqkegdfr--keinkw-----wnnlsdqgrtvtgiiaanvlvfclwrv-------------------------------------------psiqrtmiry
HRhomboid 6       213 im------------------------------------eacaggfsssvgyp-----------------grqyyfns-------------------------------sgsssgy

ICT-1024          584 htnhphmdcvitgrpccigtkgrceitsreycdfmrgyfheatlcsqvhcmddvcgll--pfl-npevpdqfyrlwlslflhagilhclvsicfqmtvlrdleklagwhriaiiyllsg
HRhomboid 2        88 ------------------------------------------itldt-----------qilespfiyspekreeawrriisymlvhagvqhiiqmlcmqlvlqiplemvhkglrvglvylagv
HRhomboid 3       348 htqflhmdceikgrpccigtkgsceittreycefmhgyfheatlcsqvhcldkvcgll--pfl-npevpdqfyriwlslflhagvvhclvsvvfqmtilrdleklagwhriaiiflsg
HRhomboid 4       204 h-------------------------------------------------------pqiraqvwryltyifmhagiehlglnvvlgllvgvpiemvhgatriglvyvagv
HRhomboid 5       196 ftsnp---------------------------------askvlcs-----------pml-----------lstfshfslfhmaanmyvlwsfsssivnilggeqfmavylsag
HRhomboid 6       243 qdyyph-----grp-----dhyeeaprnydtytaglseeeq-------------------------leralqasl-----------------wdr-----------g

ICT-1024          701 vtqmlasaiflp----yraevgpagsqfgilaclfvelfqs-wqilarpwraff--kllavvlflftfgl-lpw--i-----------dnf-----------ahlsgflsglflsfafl
HRhomboid 2       157 iaqslassiidp----lrylvgasggvyalmggyfmnvlvn-fqemipafqiff--lliiiliivldmql-aly--r-----------rffvpedqspvsfaahiaggfag--msiqyt
HRhomboid 3       465 itqmlasaiflp----yraevgpagsqfgllaclfvelfqs-wqllerpwkafl--nlsaivlflficql-lpw--i-----------dni-----------ahifgflsglllafafl
HRhomboid 4       259 vaqslavsvadm----tapvvgssgggvyalvsahlanivmn-wsgmkcqfkllr--mavalicmsmefgr-avw--lrfhpsayppcphpsfv----------ahlggvavgitlgvvvl
HRhomboid 5       254 visnfvsylgkvatgryqpslqasgaimtvlaavcckipegrlaiiflpmfttfaqnalkaiiamdtaqmilgwkff----------dha-----------ahlggalfgiw-----
HRhomboid 6       287 ntrnspp----p----ygthlspe-------------------------------------------------------------------------------------------

ICT-1024          788 pyisfqkfdlyrkrcqliifqqvvflgllaqlwvlfyvypvvrcewceflccipftdkfcekveldaqlh---
HRhomboid 2       253 vtscfdkallkdpriwiai-----------------------------aaylacvlfa-vffnifispan-----
HRhomboid 3       552 pyitfqtsdkyrkralilvsllafaqlfaalvlwlyiypinwpwiehltcfpftsrfcekveldqvlh---
HRhomboid 4       359 rn----------yeqrlqdqslwwifvamyt-vfvlfavf----wnifavtl-----------ldlklpppp
HRhomboid 5       345 -yvtygheliwknr-----------------------------eplvkiwheirtngpkkgggsk-----------
HRhomboid 6       303 ---------emrrqrl-------------------------------------------hrfdsq-----
```

FIG. 13(continued)

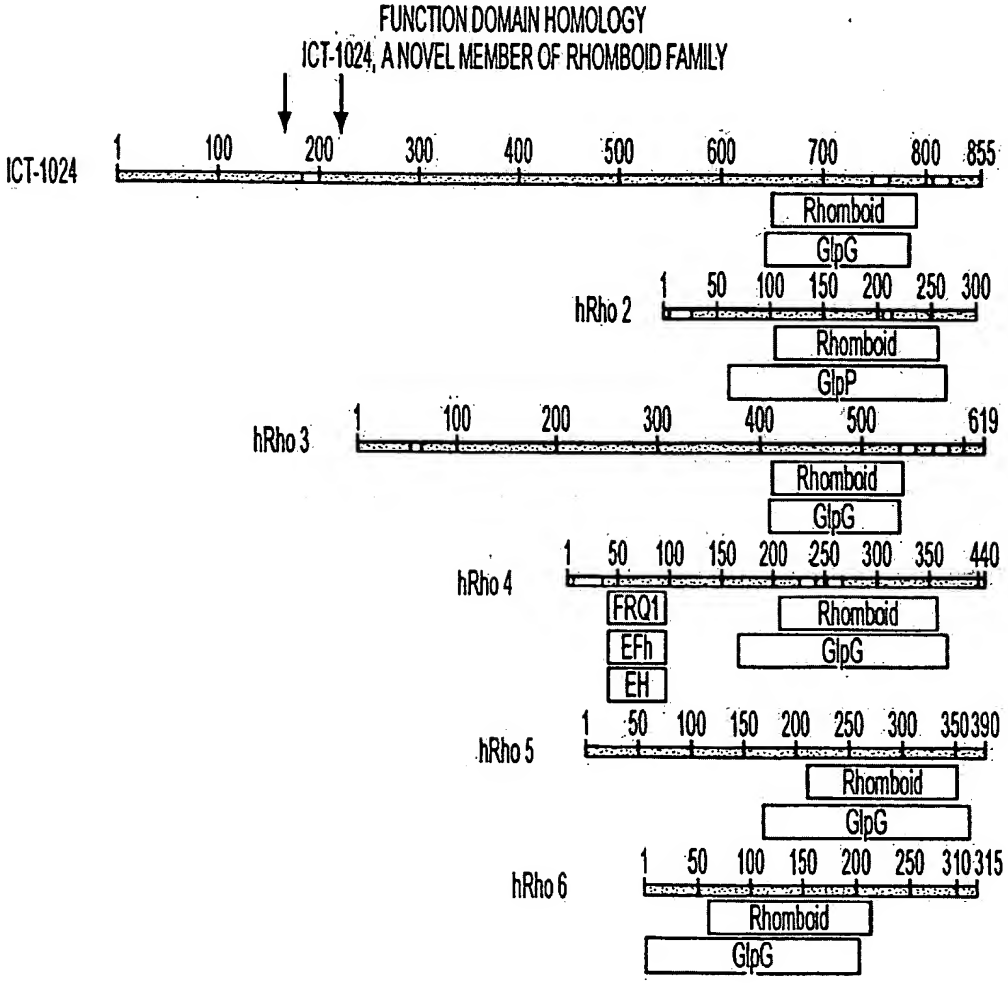

FUNCTION DOMAIN HOMOLOGY
ICT-1024, A NOVEL MEMBER OF RHOMBOID FAMILY
ICT-1024
1 100 200 300 400 500 600 700 800 855
Rhomboid
GlpG
hRho 2
1 50 100 150 200 250 300
Rhomboid
GlpP
hRho 3
1 100 200 300 400 500 619
Rhomboid
GlpG
hRho 4
1 50 100 150 200 250 300 350 440
FRQ1
EFh
EH
Rhomboid
GlpG
hRho 5
1 50 100 150 200 250 300 350 390
Rhomboid
GlpG
hRho 6
1 50 100 150 200 250 310 315
Rhomboid
GlpG

FIG. 14

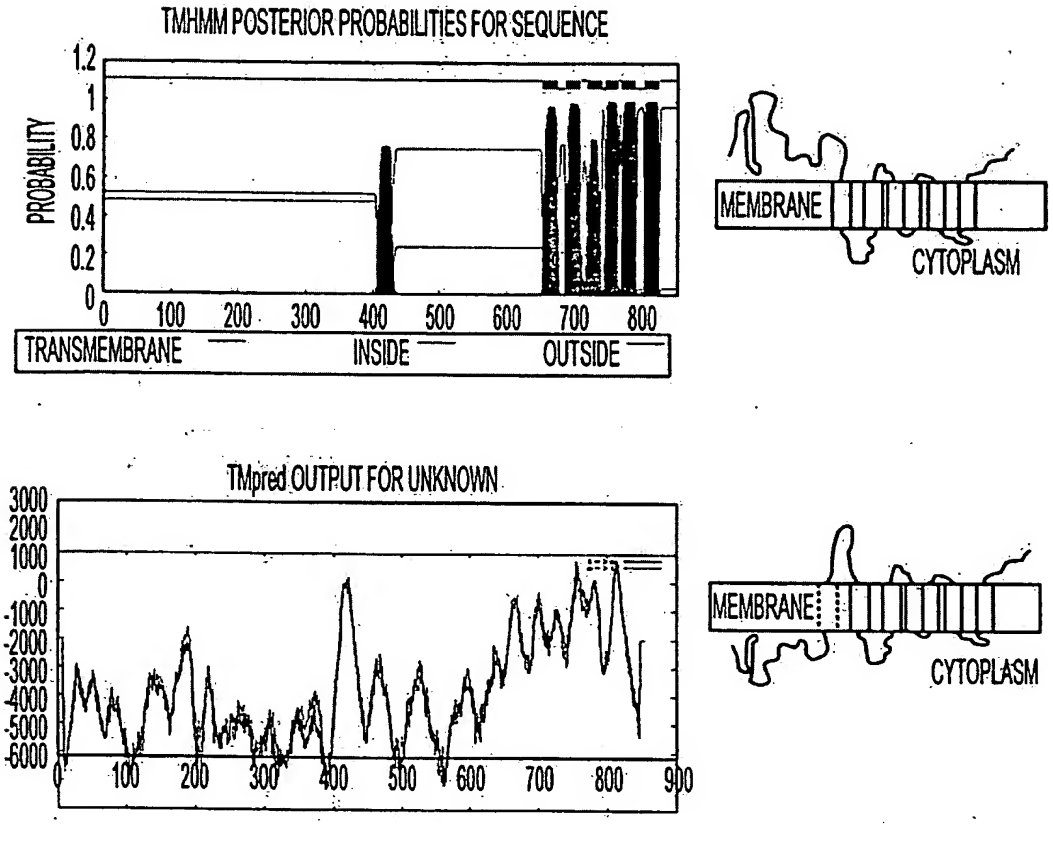

TMHMM POSTERIOR PROBABILITIES FOR SEQUENCE
PROBABILITY
1.2
1
0.8
0.6
0.4
0.2
0
0 100 200 300 400 500 600 700 800
TRANSMEMBRANE
INSIDE
OUTSIDE
MEMBRANE
CYTOPLASM
TMpred OUTPUT FOR UNKNOWN
3000
2000
1000
0
-1000
-2000
-3000
-4000
-5000
-6000
0 100 200 300 400 500 600 700 800 900
MEMBRANE
CYTOPLASM

FIG. 15

ACTIVATION OF EGFRS AND LIGANDS

ICT-1024 INTRAMEMBRANE PROTEASE ACTIVITY

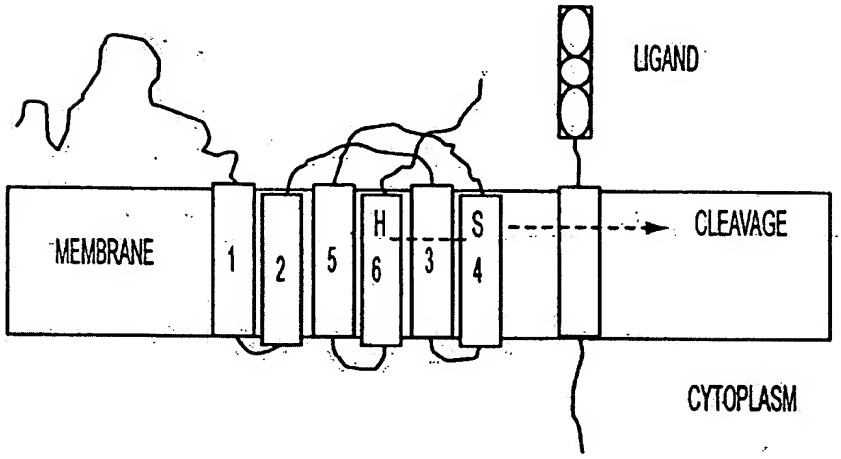


FIG. 16

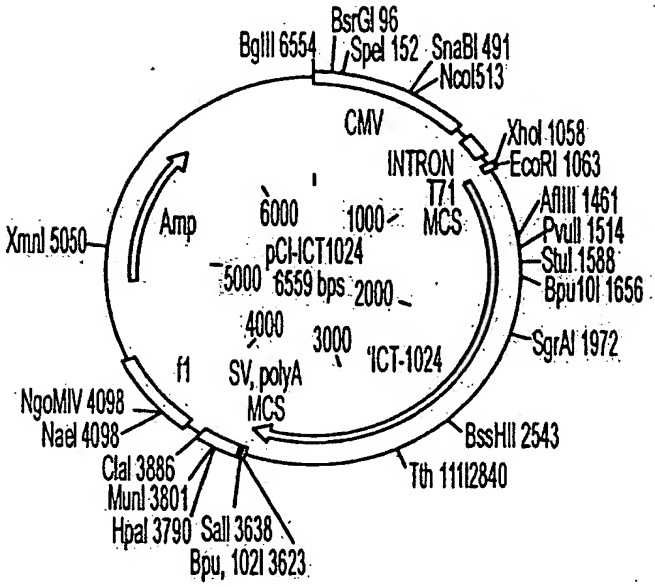

BsrGI 96
BglII 6554
SpeI 152
SnaBI 491
NcoI513
CMV
XhoI 1058
INTRON
EcoRI 1063
T71
AflIII 1461
Amp
6000
1000
MCS
PvuII 1514
XmnI 5050
pCI-ICT1024
StuI 1588
5000
6559 bps
2000
Bpu10I 1656
4000
3000
SgrAI 1972
'ICT-1024
f1
SV, polyA
MCS
NgoMIV 4098
NaeI 4098
BssHII 2543
ClaI 3886
Tth 111I2840
MunI 3801
HpaI 3790
SalI 3638
Bpu, 102I 3623

FIG. 17

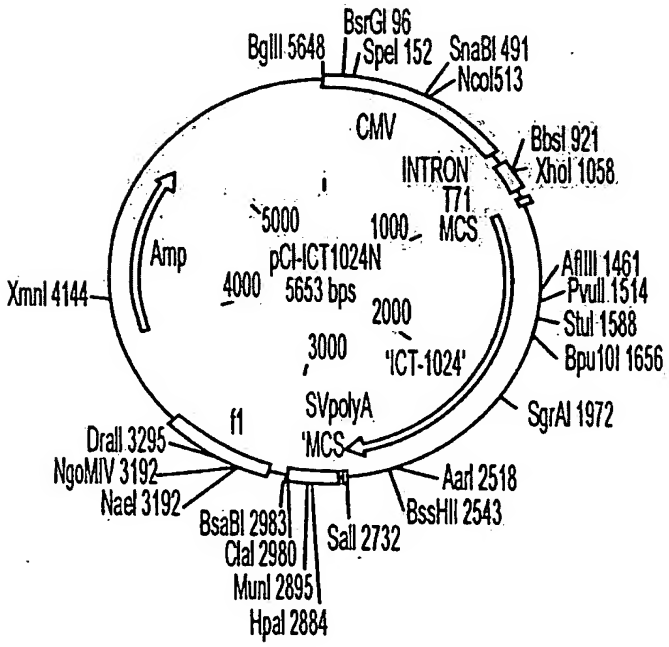

BsrGI 96
BglII 5648
SpeI 152
SnaBI 491
NcoI513
CMV
BbsI 921
INTRON
XhoI 1058
T71
5000
1000
MCS
Amp
pCI-ICT1024N
AflIII 1461
4000
5653 bps
PvuII 1514
XmnI 4144
2000
StuI 1588
3000
'ICT-1024'
Bpu10I 1656
SVpolyA
SgrAI 1972
f1
'MCS
DraII 3295
NgoMIV 3192
AarI 2518
NaeI 3192
BssHII 2543
BsaBI 2983
SalI 2732
ClaI 2980
MunI 2895
HpaI 2884

FIG. 18

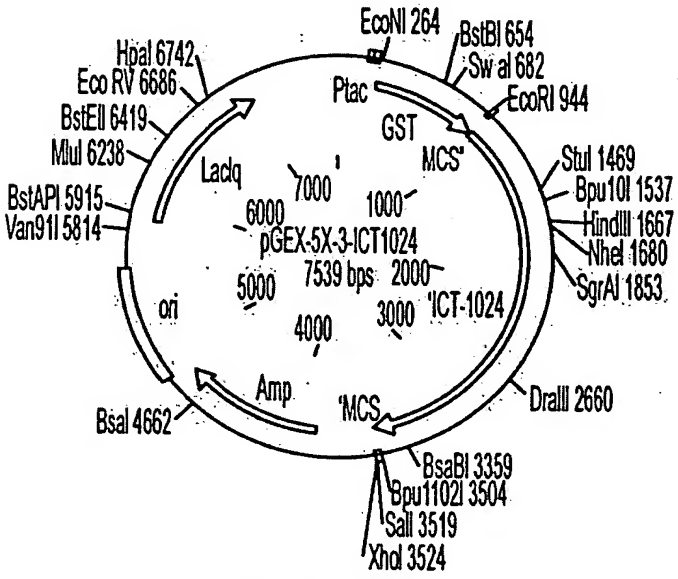
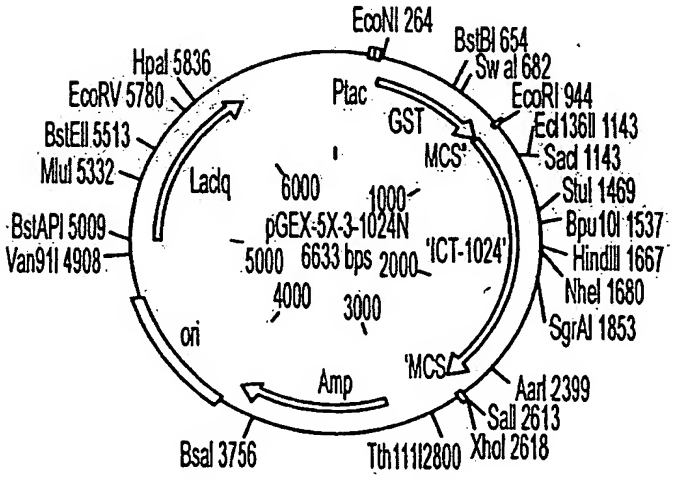

EcoNI 264
BstBI 654
Sw al 682
EcoRI 944
Ptac
GST
MCS'
Stul 1469
Bpu10I 1537
HindIII 1667
NheI 1680
SgrAI 1853
LacIq
7000
1000
6000
pGEX-5X-3-ICT1024
7539 bps
2000
5000
3000
'ICT-1024
4000
ori
Amp
'MCS
DraIII 2660
BsaI 4662
BsaBI 3359
Bpu1102I 3504
SalI 3519
XhoI 3524
HpaI 6742
Eco RV 6686
BstEII 6419
MluI 6238
BstAPI 5915
Van91I 5814

FIG. 19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BstBI 654
Sw al 682
EcoRI 944
Ptac
GST
MCS'
Ecl136II 1143
SacI 1143
StuI 1469
Bpu10I 1537
HindIII 1667
NheI 1680
SgrAI 1853
LacIq
6000
1000
pGEX-5X-3-1024N
5000
6633 bps
2000
'ICT-1024'
4000
3000
ori
Amp
'MCS
AarI 2399
SalI 2613
XhoI 2618
Tth111I2800
BsaI 3756
HpaI 5836
EcoRV 5780
BstEII 5513
MluI 5332
BstAPI 5009
Van91I 4908

FIG. 20

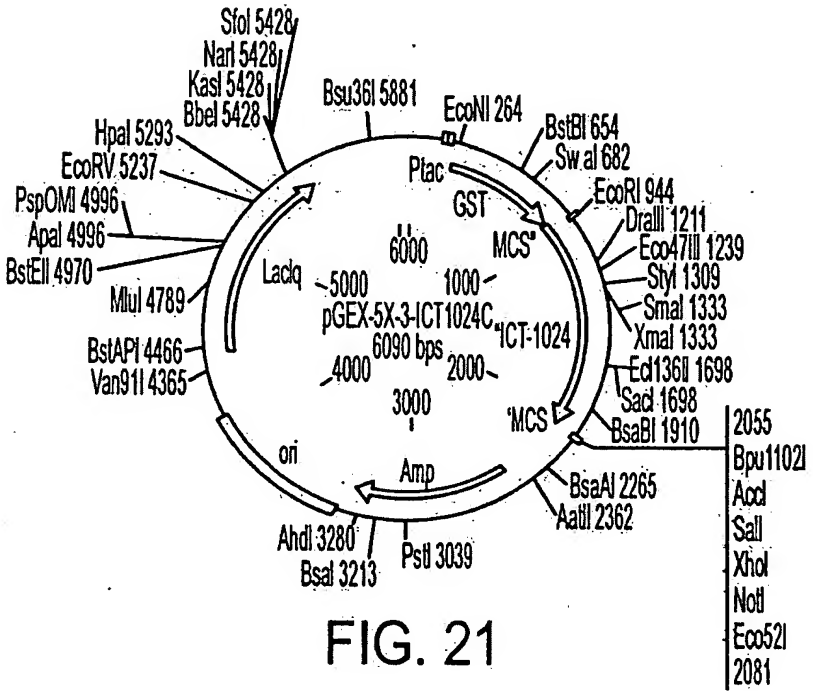
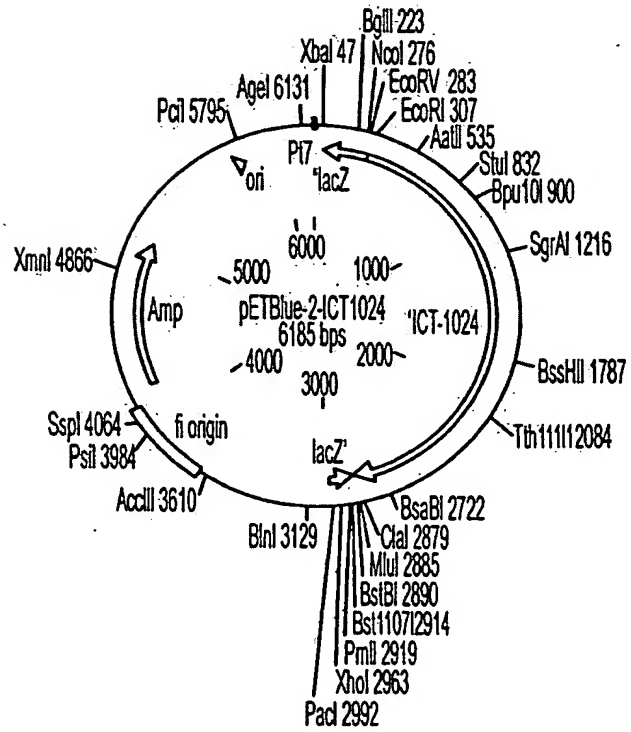

SfoI 5428
NarI 5428
KasI 5428
BbeI 5428
Bsu36I 5881
EcoNI 264
BstBI 654
SwaI 682
HpaI 5293
EcoRV 5237
PspOMI 4996
ApaI 4996
BstEII 4970
MluI 4789
BstAPI 4466
Van91I 4365
Ptac
GST
MCS'
EcoRI 944
DraIII 1211
Eco47III 1239
SfiI 1309
SmaI 1333
XmaI 1333
Ecl136II 1698
SacI 1698
BsaBI 1910
2055
Bpu1102I
AccI
SalI
XhoI
NotI
Eco52I
2081
LacIq
6000
5000
1000
pGEX-5X-3-ICT1024C
6090 bps
'ICT-1024
4000
2000
3000
'MCS
ori
Amp
BsaAI 2265
AatII 2362
AhdI 3280
BsaI 3213
PstI 3039

FIG. 21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XbaI 47
NcoI 276
AgeI 6131
EcoRV 283
PciI 5795
EcoRI 307
AatII 535
PT7
StuI 832
ori
'lacZ
Bpu10I 900
6000
SgrAI 1216
XmnI 4866
5000
1000
Amp
pETBlue-2-ICT1024
'ICT-1024
6185 bps
4000
2000
BssHII 1787
3000
SspI 4064
fi origin
Tth111II 2084
PsiI 3984
lacZ'
AccIII 3610
BsaBI 2722
BlnI 3129
ClaI 2879
MluI 2885
BstBI 2890
Bst1107I 2914
PmlI 2919
XhoI 2963
PacI 2992

FIG. 22

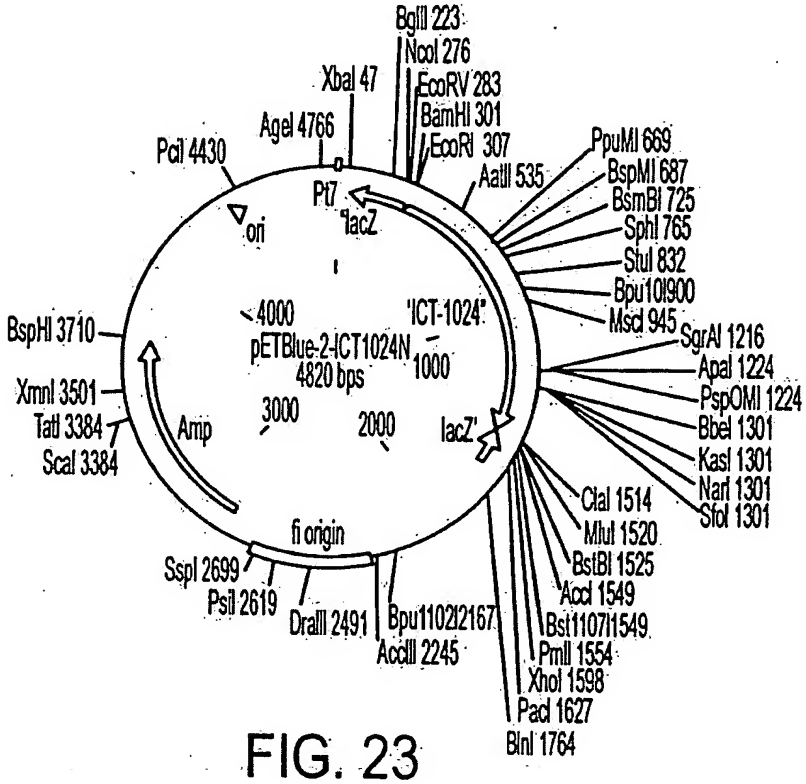
BglII 223
NcoI 276
XbaI 47
EcoRV 283
BamHI 301
AgeI 4766
EcoRI 307
PciI 4430
AatII 535
PpuMI 669
BspMI 687
BsmBI 725
SphI 765
PI7
lacZ
ori
StuI 832
Bpu10I900
MscI 945
4000
'ICT-1024'
SgrAI 1216
BspHI 3710
pETBlue-2-ICT1024N
4820 bps
1000
ApaI 1224
XmnI 3501
PspOMI 1224
3000
2000
BbeI 1301
TatI 3384
Amp
lacZ'
KasI 1301
ScaI 3384
NarI 1301
SfoI 1301
ClaI 1514
MluI 1520
fi origin
BstBI 1525
SspI 2699
AccI 1549
PsiI 2619
DraIII 2491
Bpu1102I2167
Bst1107I1549
AccIII 2245
PmlI 1554
XhoI 1598
PacI 1627
BlnI 1764

FIG. 23

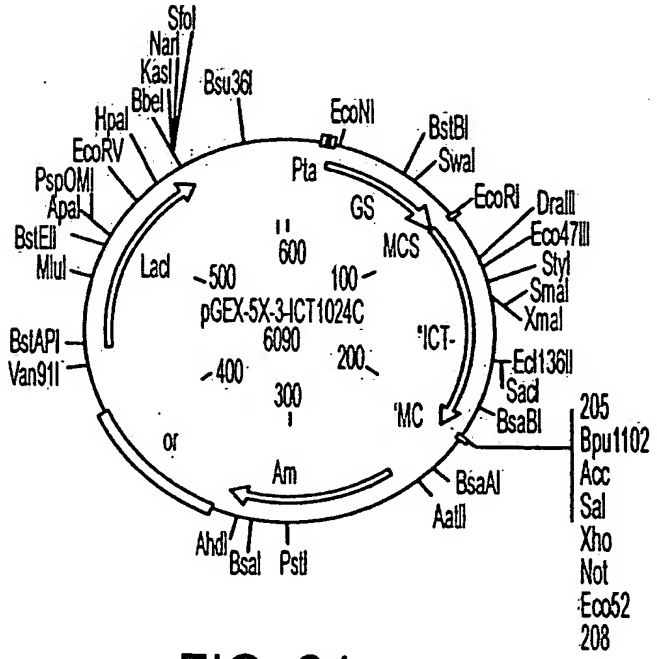
SfoI
NarI
KasI
Bsu36I
BbeI
EcoNI
HpaI
BstBI
EcoRV
SwaI
PspOMI
Pta
ApaI
GS
EcoRI
DraIII
BstEII
MCS
Eco47III
MluI
LacI
600
StyI
500
100
SmaI
pGEX-5X-3-ICT1024C
XmaI
6090
BstAPI
'ICT-
200
Van91I
400
Ecl136II
SacI
300
'MC
BsaBI
205
or
Bpu1102
Acc
Am
BsaAI
Sal
AatII
Xho
AhdI
Not
BsaI
PstI
Eco52
208

FIG. 24

(SEQ ID NO:58) ICT1024 PROTEIN (855 AA) CODING REGION: 1670-3637

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   1 TCAATATTGG CCATTAGCCA TATTATTCAT TGGTTATATA GCATAAATCA ATATTGGCTA
  61 TTGGCCATTG CATACGTTGT ATCTATATCA TAATATGTAC ATTTATATTG GCTCATGTCC
 121 AATATGACCG CCATGTTGGC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG
 181 GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC
 241 GCCTGGCTGA CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
 301 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC
 361 CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCCTATTG ACGTCAATGA
 421 CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG
 481 GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC
 541 CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT
 601 CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAATAACCC
 661 CGCCCCGTTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC
 721 TCGTTTAGTG AACCGTCAGA TCACTAGAAG CTTTATTGCG GTAGTTTATC ACAGTTAAAT
 781 TGCTAACGCA GTCAGTGCTT CTGACACAAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC
 841 GTGAGGCACT GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA
 901 ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA TTGGTCTTAC
 961 TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC CAGTTCAATT ACAGCTCTTA
1021 AGGCTAGAGT ACTTAATACG ACTCACTATA GGCTAGCCTC GAGAATTCCA TGAGTGAGGC
1081 CCGCAGGGAC AGCACGAGCA GCCTGCAGCG CAAGAAGCCA CCCTGGCTAA AGCTGGACAT
1141 TCCCTCTGCG GTGCCCCTGA CGGCAGAAGA GCCCAGCTTC CTGCAGCCCC TGAGGCGACA
1201 GGCTTTCCTG AGGAGTGTGA GTATGCCAGC CGAGACAGCC CACATCTCTT CACCCCACCA
1261 TGAGCTCCGG CGGCCGGTGC TGCAACGCCA GACGTCCATC ACACAGACCA TCCGCAGGGG
1321 GACCGCCGAC TGGTTTGGAG TGAGCAAGGA CAGTGACAGC ACCCAGAAAT GGCAGCGCAA
1381 GAGCATCCGT CACTGCAGCC AGCGCTACGG GAAGCTGAAG CCCCAGGTCC TCCGGGAGCT
1441 GGACCTGCCC AGCCAGGACA ACGTGTCGCT GACCAGCACC GAGACGCCAC CCCCACTCTA
1501 CGTGGGGCCA TGCCAGCTGG GCATGCAGAA GATCATAGAC CCCCTGGCCC GTGGCCGTGC
1561 CTTCCGTGTG GCAGATGACA CTGCGGAAGG CCTGAGTGCC CCACACACTC CCGTCACGCC
1621 GGGTGCTGCC TCCCTCTGCT CCTTCTCCAG CTCCCGCTCA GGTTTCCACC GGCTCCCGCG
1681 GCGGCGCAAG CGAGAGTCGG TGGCCAAGAT GAGCTTCCGG GCGGCCGCAG CGCTGATGAA
1741 AGGCCGCTCC GTTAGGGATG GCACCTTTCG CCGGGCACGG CGTCGAAGCT TCACTCCAGC
1801 TAGCTTTCTG GAGGAGGACA CAACTGATTT CCCCGATGAG CTGGACACAT CCTTCTTTGC
1861 CCGGGAAGGT ATCCTCCATG AAGAGCTGTC CACATACCCG GATGAAGTTT TCGAGTCCCC
1921 ATCGGAGGCA GCGCTAAAGG ACTGGGAGAA GGCACCGGAG CAGGCGGACC TCACCGGCGG
1981 GGCCCTGGAC CGCAGCGAGC TTGAGCGCAG CCACCTGATG CTGCCCTTGG AGCGAGGCTG
2041 GCGGAAGCAG AAGGAGGGCG CCGCAGCCCC GCAGCCCAAG GTGCGGCTCC GACAGGAGGT
2101 GGTGAGCACC GCGGGGCCGC GACGGGGCCA GCGTATCGCG GTGCCGGTGC GCAAGCTCTT
```

FIG. 25

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2161  CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA
2221  CCGCAAGCGC ATCGACAGCT TCGTCAAGCG CCAGATCGAG GACATGGACG ACCACAGGCC
2281  CTTCTTCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT
2341  CTATGGCATC GCGCCCGTGG GCTTCTCGCA GCATGAGACG GTGGACTCGG TGCTGCGGAA
2401  CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG
2461  CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA
2521  GGTGCACAGC TTCATTCGCT CGGCGCGCGA GCGCGAGAAG CACTCCGCCT GCTGCGTGCG
2581  CAACGACAGG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT
2641  GTGGGTGAAG TGGCCCATCC ATCCCAGCGC CCCAGAGCTT GCGGGCCACA AGAGACAGTT
2701  TGGCTCTGTC TGCCACCAGG ATCCCAGGGT GTGTGATGAG CCCTCCTCCG AAGACCCTCA
2761  TGAGTGGCCA GAAGACATCA CCAAGTGGCC GATCTGCACC AAAAACAGCG CTGGGAACCA
2821  CACCAACCAT CCCCACATGG ACTGTGTCAT CACAGGACGG CCCTGCTGCA TTGGCACCAA
2881  GGGCAGGTGT GAGATCACCT CCCGGGAGTA CTGTGACTTC ATGAGGGGCT ACTTCCATGA
2941  GGAGGCCACG CTCTGCTCTC AGGTGCACTG CATGGATGAT GTGTGTGGGC TCCTGCCTTT
3001  TCTCAACCCC GAGGTGCCTG ACCAGTTCTA CCGCCTGTGG CTATCCCTCT TCCTGCACGC
3061  CGGGATCTTG CACTGCCTGG TGTCCATCTG CTTCCAGATG ACTGTCCTGC GGGACCTGGA
3121  GAAGCTGGCA GGCTGGCACC GCATAGCCAT CATCTACCTG CTGAGTGGTG TCACCGGCAA
3181  CCTGGCCAGT GCCATCTTCC TGCCATACCG AGCAGAGGTG GGTCCTGCTG GCTCCCAGTT
3241  CGGCATCCTG GCCTGCCTCT TCGTGGAGCT CTTCCAGAGC TGGCAGATCC TGGCGCGGCC
3301  CTGGCGTGCC TTCTTCAAGC TGCTGGCTGT GGTGCTCTTC CTCTTCACCT TTGGGCTGCT
3361  GCCGTGGATT GACAACTTTG CCCACATCTC GGGGTTCATC AGTGGCCTCT TCCTCTCCTT
3421  CGCCTTCTTG CCCTACATCA GCTTTGGCAA GTTCGACCTG TACCGGAAAC GCTGCCAGAT
3481  CATCATCTTT CAGGTGGTCT TCCTGGGCCT CCTGGCTGGC CTGGTGGTCC TCTTCTACGT
3541  CTATCCTGTC CGCTGTGAGT GGTGTGAGTT CCTCACCTGC ATCCCCTTCA CTGACAAGTT
3601  CTGTGAGAAG TACGAACTGG ACGCTCAGCT CCACTGAGTC GACCCGGGCG GCCGCTTCGA
3661  GCAGACATGA TAAGATACAT TGATGAGTTT GGACAAACCA CAACTAGAAT GCAGTGAAAA
3721  AAATGCTTTA TTTGTGAAAT TTGTGATGCT ATTGCTTTAT TTGTAACCAT TATAAGCTGC
3781  AATAAACAAG TTAACAACAA CAATTGCATT CATTTTATGT TTCAGGTTCA GGGGGAGATG
3841  TGGGAGGTTT TTTAAAGCAA GTAAAACCTC TACAAATGTG GTAAAATCGA TAAGGATCCG
3901  GGCTGGCGTA ATAGCGAAGA GGCCCGCACC GATCGCCCTT CCCAACAGTT GCGCAGCCTG
3961  AATGGCGAAT GGACGCGCCC TGTAGCGGCG CATTAAGCGC GGCGGGTGTG GTGGTTACGC
4021  GCAGCGTGAC CGCTACACTT GCCAGCGCCC TAGCGCCCGC TCCTTTCGCT TTCTTCCCTT
4081  CCTTTCTCGC CACGTTCGCC GGCTTTCCCC GTCAAGCTCT AAATCGGGGG CTCCCTTTAG
4141  GGTTCCGATT TAGAGCTTTA CGGCACCTCG ACCGCAAAAA ACTTGATTTG GGTGATGGTT
4201  CACGTAGTGG GCCATCGCCC TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT
4261  TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT
4321  CTTTTGATTT ATAAGGGATT TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT
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FIG. 25 (continued)

```
4381  AACAAATATT TAACGCGAAT TTTAACAAAA TATTAACGTT TACAATTTCG CCTGATGCGG
4441  TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATGGTGCAC TCTCAGTACA
4501  ATCTGCTCTG ATGCCGCATA GTTAAGCCAG CCCCGACACC CGCCAACACC CGCTGACGCG
4561  CCCTGACGGG CTTGTCTGCT CCCGGCATCC GCTTACAGAC AAGCTGTGAC CGTCTCCGGG
4621  AGCTGCATGT GTCAGAGGTT TTCACCGTCA TCACCGAAAC GCGCGAGACG AAAGGGCCTC
4681  GTGATACGCC TATTTTTATA GGTTAATGTC ATGATAATAA TGGTTTCTTA GACGTCAGGT
4741  GGCACTTTTC GGGGAAATGT GCGCGGAACC CCTATTTGTT TATTTTTCTA AATACATTCA
4801  AATATGTATC CGCTCATGAG ACAATAACCC TGATAAATGC TTCAATAATA TTGAAAAAGG
4861  AAGAGTATGA GTATTCAACA TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC
4921  CTTCCTGTTT TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG
4981  GGTGCACGAG TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT TGAGAGTTTT
5041  CGCCCCGAAG AACGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA
5101  TTATCCCGTA TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA TTCTCAGAAT
5161  GACTTGGTTG AGTACTCACC AGTCACAGAA AAGCATCTTA CGGATGGCAT GACAGTAAGA
5221  GAATTATGCA GTGCTGCCAT AACCATGAGT GATAACACTG CGGCCAACTT ACTTCTGACA
5281  ACGATCGGAG GACCGAAGGA GCTAACCGCT TTTTTGCACA ACATGGGGGA TCATGTAACT
5341  CGCCTTGATC GTTGGGAACC GGAGCTGAAT GAAGCCATAC CAAACGACGA GCGTGACACC
5401  ACGATGCCTG TAGCAATGGC AACAACGTTG CGCAAACTAT TAACTGGCGA ACTACTTACT
5461  CTAGCTTCCC GGCAACAATT AATAGACTGG ATGGAGGCGG ATAAAGTTGC AGGACCACTT
5521  CTGCGCTCGG CCCTTCCGGC TGGCTGGTTT ATTGCTGATA AATCTGGAGC CGGTGAGCGT
5581  GGGTCTCGCG GTATCATTGC AGCACTGGGG CCAGATGGTA AGCCCTCCCG TATCGTAGTT
5641  ATCTACACGA CGGGGAGTCA GGCAACTATG GATGAACGAA ATAGACAGAT CGCTGAGATA
5701  GGTGCCTCAC TGATTAAGCA TTGGTAACTG TCAGACCAAG TTTACTCATA TATACTTTAG
5761  ATTGATTTAA AACTTCATTT TTAATTTAAA AGGATCTAGG TGAAGATCCT TTTTGATAAT
5821  CTCATGACCA AAATCCCTTA ACGTGAGTTT TCGTTCCACT GAGCGTCAGA CCCCGTAGAA
5881  AAGATCAAAG GATCTTCTTG AGATCCTTTT TTTCTGCGCG TAATCTGCTG CTTGCAAACA
5941  AAAAAACCAC CGCTACCAGC GGTGGTTTGT TTGCCGGATC AAGAGCTACC AACTCTTTTT
6001  CCGAAGGTAA CTGGCTTCAG CAGAGCGCAG ATACCAAATA CTGTCCTTCT AGTGTAGCCG
6061  TAGTTAGGCC ACCACTTCAA GAACTCTGTA GCACCGCCTA CATACCTCGC TCTGCTAATC
6121  CTGTTACCAG TGGCTGCTGC CAGTGGCGAT AAGTCGTGTC TTACCGGGTT GGACTCAAGA
6181  CGATAGTTAC CGGATAAGGC GCAGCGGTCG GGCTGAACGG GGGGTTCGTG CACACAGCCC
6241  AGCTTGGAGC GAACGACCTA CACCGAACTG AGATACCTAC AGCGTGAGCT ATGAGAAAGC
6301  GCCACGCTTC CCGAAGGGAG AAAGGCGGAC AGGTATCCGG TAAGCGGCAG GGTCGGAACA
6361  GGAGAGCGCA CGAGGGAGCT TCCAGGGGGA AACGCCTGGT ATCTTTATAG TCCTGTCGGG
6421  TTTCGCCACC TCTGACTTGA GCGTCGATTT TTGTGATGCT CGTCAGGGGG GCGGAGCCTA
6481  TGGAAAAACG CCAGCAACGC GGCCTTTTTA CGGTTCCTGG CCTTTTGCTG GCCTTTTGCT
6541  CACATGGCTC GACAGATCT
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FIG. 25 (continued)

(SEQ ID NO:60) ICT1024 N TERMINUS 553 AA CODING REGION: 1070-2731

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   1 TCAATATTGG CCATTAGC CA TATTATTCAT TGGTTATATA GCATAAATCA ATATTGGCTA
  61 TTGGCCATTG CATACGTTGT ATCTATATCA TAATATGTAC ATTTATATTG GCTCATGTCC
 121 AATATGACCG CCATGTTGGC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG
 181 GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC
 241 GCCTGGCTGA CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
 301 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC
 361 CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCCTATTG ACGTCAATGA
 421 CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG
 481 GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC
 541 CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT
 601 CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAATAACCC
 661 CGCCCCGTTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC
 721 TCGTTTAGTG AACCGTCAGA TCACTAGAAG CTTTATTGCG GTAGTTTATC ACAGTTAAAT
 781 TGCTAACGCA GTCAGTGCTT CTGACACAAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC
 841 GTGAGGCACT GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA
 901 ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA TTGGTCTTAC
 961 TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC CAGTTCAATT ACAGCTCTTA
1021 AGGCTAGAGT ACTTAATACG ACTCACTATA GGCTAGCCTC GAGAATTCCA TGAGTGAGGC
1081 CCGCAGGGAC AGCACGAGCA GCCTGCAGCG CAAGAAGCCA CCCTGGCTAA AGCTGGACAT
1141 TCCCTCTGCG GTGCCCCTGA CGGCAGAAGA GCCCAGCTTC CTGCAGCCCC TGAGGCGACA
1201 GGCTTTCCTG AGGAGTGTGA GTATGCCAGC CGAGACAGCC CACATCTCTT CACCCCACCA
1261 TGAGCTCCGG CGGCCGGTGC TGCAACGCCA GACGTCCATC ACACAGACCA TCCGCAGGGG
1321 GACCGCCGAC TGGTTTGGAG TGAGCAAGGA CAGTGACAGC ACCCAGAAAT GGCAGCGCAA
1381 GAGCATCCGT CACTGCAGCC AGCGCTACGG GAAGCTGAAG CCCCAGGTCC TCCGGGAGCT
1441 GGACCTGCCC AGCCAGGACA ACGTGTCGCT GACCAGCACC GAGACGCCAC CCCCACTCTA
1501 CGTGGGGCCA TGCCAGCTGG GCATGCAGAA GATCATAGAC CCCCTGGCCC GTGGCCGTGC
1561 CTTCCGTGTG GCAGATGACA CTGCGGAAGG CCTGAGTGCC CCACACACTC CCGTCACGCC
1621 GGGTGCTGCC TCCCTCTGCT CCTTCTCCAG CTCCCGCTCA GGTTTCCACC GGCTCCCGCG
1681 GCGGCGCAAG CGAGAGTCGG TGGCCAAGAT GAGCTTCCGG GCGGCCGCAG CGCTGATGAA
1741 AGGCCGCTCC GTTAGGGATG GCACCTTTCG CCGGGCACGG CGTCGAAGCT TCACTCCAGC
1801 TAGCTTTCTG GAGGAGGACA CAACTGATTT CCCCGATGAG CTGGACACAT CCTTCTTTGC
1861 CCGGGAAGGT ATCCTCCATG AAGAGCTGTC CACATACCCG GATGAAGTTT TCGAGTCCCC
1921 ATCGGAGGCA GCGCTAAAGG ACTGGGAGAA GGCACCGGAG CAGGCGGACC TCACCGGCGG
1981 GGCCCTGGAC CGCAGCGAGC TTGAGCGCAG CCACCTGATG CTGCCCTTGG AGCGAGGCTG
2041 GCGGAAGCAG AAGGAGGGCG CCGCAGCCCC GCAGCCCAAG GTGCGGCTCC GACAGGAGGT
2101 GGTGAGCACC GCGGGGCCGC GACGGGGCCA GCGTATCGCG GTGCCGGTGC GCAAGCTCTT
```

FIG. 26

2161 CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA
2221 CCGCAAGCGC ATCGACAGCT TCGTCAAGCG CCAGATCGAG GACATGGACG ACCACAGGCC
2281 CTTCTTCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT
2341 CTATGGCATC GCGCCCGTGG GCTTCTCGCA GCATGAGACG GTGGACTCGG TGCTGCGGAA
2401 CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG
2461 CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA
2521 GGTGCACAGC TTCATTCGCT CGGCGCGCGA GCGCGAGAAG CACTCCGCCT GCTGCGTGCG
2581 CAACGACAGG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT
2641 GTGGGTGAAG TGGCCCATCC ATCCCAGCGC CCCAGAGCTT GCGGGCCACA AGAGACAGTT
2701 TGGCTCTGTC TGCCACCAGG ATCCCAGGTG AGTCGACCCG GGCGGCCGCT TCGAGCAGAC
2761 ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA GAATGCAGTG AAAAAAATGC
2821 TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG CTGCAATAAA
2881 CAAGTTAACA ACAACAATTG CATTCATTTT ATGTTTCAGG TTCAGGGGGA GATGTGGGAG
2941 GTTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTAAAA TCGATAAGGA TCCGGGCTGG
3001 CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC
3061 GAATGGACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT ACGCGCAGCG
3121 TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTTCTTC CCTTCCTTTC
3181 TCGCCACGTT CGCCGGCTTT CCCCGTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC
3241 GATTTAGAGC TTTACGGCAC CTCGACCGCA AAAAACTTGA TTTGGGTGAT GGTTCACGTA
3301 GTGGGCCATC GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA
3361 ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATTCTTTTG
3421 ATTTATAAGG GATTTTGCCG ATTTCGGCCT ATTGGTTAAA AAATGAGCTG ATTTAACAAA
3481 TATTTAACGC GAATTTTAAC AAAATATTAA CGTTTACAAT TTCGCCTGAT GCGGTATTTT
3541 CTCCTTACGC ATCTGTGCGG TATTTCACAC CGCATATGGT GCACTCTCAG TACAATCTGC
3601 TCTGATGCCG CATAGTTAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA
3661 CGGGCTTGTC TGCTCCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC CGGGAGCTGC
3721 ATGTGTCAGA GGTTTTCACC GTCATCACCG AAACGCGCGA GACGAAAGGG CCTCGTGATA
3781 CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT
3841 TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG
3901 TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT
3961 ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT
4021 GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA
4081 CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC
4141 GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC
4201 CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG
4261 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA
4321 TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC

FIG. 26 (continued)

4381 GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
4441 GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG
4501 CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT
4561 TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC
4621 TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT
4681 CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC
4741 ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC
4801 TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
4861 TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG
4921 ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC
4981 AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA
5041 CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG
5101 GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
5161 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA
5221 CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG
5281 TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG
5341 GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG
5401 CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
5461 CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC
5521 CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA
5581 AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG
5641 GCTCGACAGA TCT

FIG. 26 (continued)

(SEQ ID NO: 61) ICT1024 coding region: 947-3518

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   1  TCGACTCGAG CGGCCGCATC GTGACTGACT GACGATCTGC CTCGCGCGTT TCGGTGATGA
  61  CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA
 121  TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC
 181  AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATAAT TCTTGAAGAC GAAAGGGCCT
 241  CGTGATACGC CTATTTTTAT AGGTTAATGT CATGATAATA ATGGTTTCTT AGACGTCAGG
 301  TGGCACTTTT CGGGGAAATG TGCGCGGAAC CCCTATTTGT TTATTTTTCT AAATACATTC
 361  AAATATGTAT CCGCTCATGA GACAATAACC CTGATAAATG CTTCAATAAT ATTGAAAAAG
 421  GAAGAGTATG AGTATTCAAC ATTTCCGTGT CGCCCTTATT CCCTTTTTTG CGGCATTTTG
 481  CCTTCCTGTT TTTGCTCACC CAGAAACGCT GGTGAAAGTA AAAGATGCTG AAGATCAGTT
 541  GGGTGCACGA GTGGGTTACA TCGAACTGGA TCTCAACAGC GGTAAGATCC TTGAGAGTTT
 601  TCGCCCCGAA GAACGTTTTC CAATGATGAG CACTTTTAAA GTTCTGCTAT GTGGCGCGGT
 661  ATTATCCCGT GTTGACGCCG GGCAAGAGCA ACTCGGTCGC CGCATACACT ATTCTCAGAA
 721  TGACTTGGTT GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG
 781  AGAATTATGC AGTGCTGCCA TAACCATGAG TGATAACACT GCGGCCAACT TACTTCTGAC
 841  AACGATCGGA GGACCGAAGG AGCTAACCGC TTTTTTGCAC AACATGGGGG ATCATGTAAC
 901  TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA TGAAGCCATA CCAAACGACG AGCGTGACAC
 961  CACGATGCCT GCAGCAATGG CAACAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC
1021  TCTAGCTTCC CGGCAACAAT TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT
1081  TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG
1141  TGGGTCTCGC GGTATCATTG CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT
1201  TATCTACACG ACGGGGAGTC AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT
1261  AGGTGCCTCA CTGATTAAGC ATTGGTAACT GTCAGACCAA GTTTACTCAT ATATACTTTA
1321  GATTGATTTA AAACTTCATT TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTTTGATAA
1381  TCTCATGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA
1441  AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC
1501  AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT
1561  TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC
1621  GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT
1681  CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG
1741  ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC
1801  CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG
1861  CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC
1921  AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG
1981  GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGAGCCT
2041  ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC
2101  TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA
```

FIG. 27

2161 GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA
2221 AGCGGAAGAG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG
2281 CATAAATTCC GACACCATCG AATGGTGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC
2341 GGAAGAGAGT CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG ATGTCGCAGA
2401 GTATGCCGGT GTCTCTTATC AGACCGTTTC CCGCGTGGTG AACCAGGCCA GCCACGTTTC
2461 TGCGAAAACG CGGGAAAAAG TGGAAGCGGC GATGGCGGAG CTGAATTACA TTCCCAACCG
2521 CGTGGCACAA CAACTGGCGG GCAAACAGTC GTTGCTGATT GGCGTTGCCA CCTCCAGTCT
2581 GGCCCTGCAC GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG
2641 TGCCAGCGTG GTGGTGTCGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT
2701 GCACAATCTT CTCGCGCAAC GCGTCAGTGG GCTGATCATT AACTATCCGC TGGATGACCA
2761 GGATGCCATT GCTGTGGAAG CTGCCTGCAC TAATGTTCCG GCGTTATTTC TTGATGTCTC
2821 TGACCAGACA CCCATCAACA GTATTATTTT CTCCCATGAA GACGGTACGC GACTGGGCGT
2881 GGAGCATCTG GTCGCATTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAGTTC
2941 TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA ATCAAATTCA
3001 GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA
3061 AATGCTGAAT GAGGGCATCG TTCCCACTGC GATGCTGGTT GCCAACGATC AGATGGCGCT
3121 GGGCGCAATG CGCGCCATTA CCGAGTCCGG GCTGCGCGTT GGTGCGGATA TCTCGGTAGT
3181 GGGATACGAC GATACCGAAG ACAGCTCATG TTATATCCCG CCGTTAACCA CCATCAAACA
3241 GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA
3301 GGCGGTGAAG GGCAATCAGC TGTTGCCCGT CTCACTGGTG AAAAGAAAAA CCACCCTGGC
3361 GCCCAATACG CAAACCGCCT CTCCCCGCGC GTTGGCCGAT TCATTAATGC AGCTGGCACG
3421 ACAGGTTTCC CGACTGGAAA GCGGGCAGTG AGCGCAACGC AATTAATGTG AGTTAGCTCA
3481 CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG TGTGGAATTG
3541 TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA TGATTACGGA TTCACTGGCC
3601 GTCGTTTTAC AACGTCGTGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA
3661 GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC
3721 CAACAGTTGC GCAGCCTGAA TGGCGAATGG CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG
3781 GTGCCGGAAA GCTGGCTGGA GTGCGATCTT CCTGAGGCCG ATACTGTCGT CGTCCCCTCA
3841 AACTGGCAGA TGCACGGTTA CGATGCGCCC ATCTACACCA ACGTAACCTA TCCCATTACG
3901 GTCAATCCGC CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT
3961 GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG CGTTGGAATT
4021 AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
4081 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
4141 TCTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
4201 TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
4261 CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
4321 AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC

FIG. 27 (continued)

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4381  GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
4441  TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
4501  TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
4561  TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
4621  TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
4681  ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
4741  TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
4801  AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
4861  CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
4921  ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGG
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FIG. 27 (continued)

(SEQ ID NO: 62) ICT1024 N terminus 553 aa coding region: 947-2600

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   1 AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
  61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
 121 TCTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
 181 TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
 241 CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
 301 AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
 361 GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
 421 TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
 481 TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
 541 TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
 601 TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
 661 ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
 721 TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
 781 AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
 841 CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
 901 ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGGAATTCC ATGAGTGAGG
 961 CCCGCAGGGA CAGCACGAGC AGCCTGCAGC GCAAGAAGCC ACCCTGGCTA AAGCTGGACA
1021 TTCCCTCTGC GGTGCCCCTG ACGGCAGAAG AGCCCAGCTT CCTGCAGCCC CTGAGGCGAC
1081 AGGCTTTCCT GAGGAGTGTG AGTATGCCAG CCGAGACAGC CCACATCTCT TCACCCCACC
1141 ATGAGCTCCG GCGGCCGGTG CTGCAACGCC AGACGTCCAT CACACAGACC ATCCGCAGGG
1201 GGACCGCCGA CTGGTTTGGA GTGAGCAAGG ACAGTGACAG CACCCAGAAA TGGCAGCGCA
1261 AGAGCATCCG TCACTGCAGC CAGCGCTACG GGAAGCTGAA GCCCCAGGTC CTCCGGGAGC
1321 TGGACCTGCC CAGCCAGGAC AACGTGTCGC TGACCAGCAC CGAGACGCCA CCCCCACTCT
1381 ACGTGGGGCC ATGCCAGCTG GGCATGCAGA AGATCATAGA CCCCCTGGCC CGTGGCCGTG
1441 CCTTCCGTGT GGCAGATGAC ACTGCGGAAG GCCTGAGTGC CCCACACACT CCCGTCACGC
1501 CGGGTGCTGC CTCCCTCTGC TCCTTCTCCA GCTCCCGCTC AGGTTTCCAC CGGCTCCCGC
1561 GGCGGCGCAA GCGAGAGTCG GTGGCCAAGA TGAGCTTCCG GGCGGCCGCA GCGCTGATGA
1621 AAGGCCGCTC CGTTAGGGAT GGCACCTTTC GCCGGGCACG GCGTCGAAGC TTCACTCCAG
1681 CTAGCTTTCT GGAGGAGGAC ACAACTGATT TCCCCGATGA GCTGGACACA TCCTTCTTTG
1741 CCCGGGAAGG TATCCTCCAT GAAGAGCTGT CCACATACCC GGATGAAGTT TTCGAGTCCC
1801 CATCGGAGGC AGCGCTAAAG GACTGGGAGA AGGCACCGGA GCAGGCGGAC CTCACCGGCG
1861 GGGCCCTGGA CCGCAGCGAG CTTGAGCGCA GCCACCTGAT GCTGCCCTTG GAGCGAGGCT
1921 GGCGGAAGCA GAAGGAGGGC GCCGCAGCCC CGCAGCCCAA GGTGCGGCTC CGACAGGAGG
1981 TGGTGAGCAC CGCGGGGCCG CGACGGGGCC AGCGTATCGC GGTGCCGGTG CGCAAGCTCT
2041 TCGCCCGGGA GAAGCGGCCG TATGGGCTGG GCATGGTGGG ACGGCTCACC AACCGCACCT
2101 ACCGCAAGCG CATCGACAGC TTCGTCAAGC GCCAGATCGA GGACATGGAC GACCACAGGC
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FIG. 28

2161 CCTTCTTCAC CTACTGGCTT ACCTTCGTGC ACTCGCTCGT CACCATCCTA GCCGTGTGCA
2221 TCTATGGCAT CGCGCCCGTG GGCTTCTCGC AGCATGAGAC GGTGGACTCG GTGCTGCGGA
2281 ACCGCGGGGT CTACGAGAAC GTCAAGTACG TGCAGCAGGA GAACTTCTGG ATCGGGCCCA
2341 GCTCGGAGGC CCTCATCCAC CTGGGCGCCA AGTTTTCGCC CTGCATGCGC CAGGACCCGC
2401 AGGTGCACAG CTTCATTCGC TCGGCGCGCG AGCGCGAGAA GCACTCCGCC TGCTGCGTGC
2461 GCAACGACAG GTCGGGCTGC GTGCAGACCT CGGAGGAGGA GTGCTCGTCC ACGCTGGCAG
2521 TGTGGGTGAA GTGGCCCATC CATCCCAGCG CCCCAGAGCT TGCGGGCCAC AAGAGACAGT
2581 TTGGCTCTGT CTGCCACCAG GATCCCAGGT GAGTCGACTC GAGCGGCCGC ATCGTGACTG
2641 ACTGACGATC TGCCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT
2701 CCCGGAGACG GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG
2761 CGCGTCAGCG GGTGTTGGCG GGTGTCGGGG CGCAGCCATG ACCCAGTCAC GTAGCGATAG
2821 CGGAGTGTAT AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA
2881 TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG
2941 AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA
3001 ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG
3061 TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC
3121 GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT
3181 GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
3241 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG CCGGGCAAGA
3301 GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC
3361 AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT
3421 GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC
3481 CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT
3541 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA TGGCAACAAC
3601 GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA
3661 CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG
3721 GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT
3781 GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC
3841 TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA
3901 ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT TTAAAACTTC ATTTTTAATT
3961 TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA
4021 GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC
4081 TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT
4141 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC
4201 GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC
4261 TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG
4321 CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG

FIG. 28 (continued)

4381 GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
4441 ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC
4501 GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG
4561 GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG
4621 ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT
4681 TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC
4741 TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG
4801 AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA GAGCGCCTGA TGCGGTATTT
4861 TCTCCTTACG CATCTGTGCG GTATTTCACA CCGCATAAAT TCCGACACCA TCGAATGGTG
4921 CAAAACCTTT CGCGGTATGG CATGATAGCG CCCGGAAGAG AGTCAATTCA GGGTGGTGAA
4981 TGTGAAACCA GTAACGTTAT ACGATGTCGC AGAGTATGCC GGTGTCTCTT ATCAGACCGT
5041 TTCCCGCGTG GTGAACCAGG CCAGCCACGT TTCTGCGAAA ACGCGGGAAA AAGTGGAAGC
5101 GGCGATGGCG GAGCTGAATT ACATTCCCAA CCGCGTGGCA CAACAACTGG CGGGCAAACA
5161 GTCGTTGCTG ATTGGCGTTG CCACCTCCAG TCTGGCCCTG CACGCGCCGT CGCAAATTGT
5221 CGCGGCGATT AAATCTCGCG CCGATCAACT GGGTGCCAGC GTGGTGGTGT CGATGGTAGA
5281 ACGAAGCGGC GTCGAAGCCT GTAAAGCGGC GGTGCACAAT CTTCTCGCGC AACGCGTCAG
5341 TGGGCTGATC ATTAACTATC CGCTGGATGA CCAGGATGCC ATTGCTGTGG AAGCTGCCTG
5401 CACTAATGTT CCGGCGTTAT TTCTTGATGT CTCTGACCAG ACACCCATCA ACAGTATTAT
5461 TTTCTCCCAT GAAGACGGTA CGCGACTGGG CGTGGAGCAT CTGGTCGCAT TGGGTCACCA
5521 GCAAATCGCG CTGTTAGCGG GCCCATTAAG TTCTGTCTCG GCGCGTCTGC GTCTGGCTGG
5581 CTGGCATAAA TATCTCACTC GCAATCAAAT TCAGCCGATA GCGGAACGGG AAGGCGACTG
5641 GAGTGCCATG TCCGGTTTTC AACAAACCAT GCAAATGCTG AATGAGGGCA TCGTTCCCAC
5701 TGCGATGCTG GTTGCCAACG ATCAGATGGC GCTGGGCGCA ATGCGCGCCA TTACCGAGTC
5761 CGGGCTGCGC GTTGGTGCGG ATATCTCGGT AGTGGGATAC GACGATACCG AAGACAGCTC
5821 ATGTTATATC CCGCCGTTAA CCACCATCAA ACAGGATTTT CGCCTGCTGG GGCAAACCAG
5881 CGTGGACCGC TTGCTGCAAC TCTCTCAGGG CCAGGCGGTG AAGGGCAATC AGCTGTTGCC
5941 CGTCTCACTG GTGAAAAGAA AAACCACCCT GGCGCCCAAT ACGCAAACCG CCTCTCCCCG
6001 CGCGTTGGCC GATTCATTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA
6061 GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT
6121 TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
6181 ACAGCTATGA CCATGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA
6241 AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC CAGCTGGCGT

FIG. 28 (continued)

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6301  AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA
6361  TGGCGCTTTG CCTGGTTTCC GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT
6421  CTTCCTGAGG CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG
6481  CCCATCTACA CCAACGTAAC CTATCCCATT ACGGTCAATC CGCCGTTTGT TCCCACGGAG
6541  AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG AAAGCTGGCT ACAGGAAGGC
6601  CAGACGCGAA TTATTTTTGA TGGCGTTGGA ATT
```

FIG. 28 (continued)

(SEQ ID NO:64) Coding region for the C terminus 375 aa: 945-2069

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   1 AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
  61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
 121 TCTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
 181 TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
 241 CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
 301 AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
 361 GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
 421 TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
 481 TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
 541 TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
 601 TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
 661 ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
 721 TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
 781 AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT
 841 CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
 901 ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGGAATTCC CAGGTGCACA
 961 GCTTCATTCG CTCGGCGCGC GAGCGCGAGA AGCACTCCGC CTGCTGCGTG CGCAACGACA
1021 GGTCGGGCTG CGTGCAGACC TCGGAGGAGG AGTGCTCGTC CACGCTGGCA GTGTGGGTGA
1081 AGTGGCCCAT CCATCCCAGC GCCCCAGAGC TTGCGGGCCA CAAGAGACAG TTTGGCTCTG
1141 TCTGCCACCA GGATCCCAGG GTGTGTGATG AGCCCTCCTC CGAAGACCCT CATGAGTGGC
1201 CAGAAGACAT CACCAAGTGG CCGATCTGCA CCAAAAACAG CGCTGGGAAC CACACCAACC
1261 ATCCCCACAT GGACTGTGTC ATCACAGGAC GGCCCTGCTG CATTGGCACC AAGGGCAGGT
1321 GTGAGATCAC CTCCCGGGAG TACTGTGACT TCATGAGGGG CTACTTCCAT GAGGAGGCCA
1381 CGCTCTGCTC TCAGGTGCAC TGCATGGATG ATGTGTGTGG GCTCCTGCCT TTTCTCAACC
1441 CCGAGGTGCC TGACCAGTTC TACCGCCTGT GGCTATCCCT CTTCCTGCAC GCCGGGATCT
1501 TGCACTGCCT GGTGTCCATC TGCTTCCAGA TGACTGTCCT GCGGGACCTG GAGAAGCTGG
1561 CAGGCTGGCA CCGCATAGCC ATCATCTACC TGCTGAGTGG TGTCACCGGC AACCTGGCCA
1621 GTGCCATCTT CCTGCCATAC CGAGCAGAGG TGGGTCCTGC TGGCTCCCAG TTCGGCATCC
1681 TGGCCTGCCT CTTCGTGGAG CTCTTCCAGA GCTGGCAGAT CCTGGCGCGG CCCTGGCGTG
1741 CCTTCTTCAA GCTGCTGGCT GTGGTGCTCT TCCTCTTCAC CTTTGGGCTG CTGCCGTGGA
1801 TTGACAACTT TGCCCACATC TCGGGGTTCA TCAGTGGCCT CTTCCTCTCC TTCGCCTTCT
1861 TGCCCTACAT CAGCTTTGGC AAGTTCGACC TGTACCGGAA ACGCTGCCAG ATCATCATCT
1921 TTCAGGTGGT CTTCCTGGGC CTCCTGGCTG GCCTGGTGGT CCTCTTCTAC GTCTATCCTG
1981 TCCGCTGTGA GTGGTGTGAG TTCCTCACCT GCATCCCCTT CACTGACAAG TTCTGTGAGA
2041 AGTACGAACT GGACGCTCAG CTCCACTGAG TCGACTCGAG CGGCCGCATC GTGACTGACT
2101 GACGATCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC
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FIG. 29

2161 GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC
2221 GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG
2281 AGTGTATAAT TCTTGAAGAC GAAAGGGCCT CGTGATACGC CTATTTTTAT AGGTTAATGT
2341 CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT CGGGGAAATG TGCGCGGAAC
2401 CCCTATTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTCATGA GACAATAACC
2461 CTGATAAATG CTTCAATAAT ATTGAAAAAG GAAGAGTATG AGTATTCAAC ATTTCCGTGT
2521 CGCCCTTATT CCCTTTTTTG CGGCATTTTG CCTTCCTGTT TTTGCTCACC CAGAAACGCT
2581 GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA GTGGGTTACA TCGAACTGGA
2641 TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA GAACGTTTTC CAATGATGAG
2701 CACTTTTAAA GTTCTGCTAT GTGGCGCGGT ATTATCCCGT GTTGACGCCG GGCAAGAGCA
2761 ACTCGGTCGC CGCATACACT ATTCTCAGAA TGACTTGGTT GAGTACTCAC CAGTCACAGA
2821 AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC AGTGCTGCCA TAACCATGAG
2881 TGATAACACT GCGGCCAACT TACTTCTGAC AACGATCGGA GGACCGAAGG AGCTAACCGC
2941 TTTTTTGCAC AACATGGGGG ATCATGTAAC TCGCCTTGAT CGTTGGGAAC CGGAGCTGAA
3001 TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCT GCAGCAATGG CAACAACGTT
3061 GCGCAAACTA TTAACTGGCG AACTACTTAC TCTAGCTTCC CGGCAACAAT TAATAGACTG
3121 GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT
3181 TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG CAGCACTGGG
3241 GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG ACGGGGAGTC AGGCAACTAT
3301 GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC ATTGGTAACT
3361 GTCAGACCAA GTTTACTCAT ATATACTTTA GATTGATTTA AAACTTCATT TTTAATTTAA
3421 AAGGATCTAG GTGAAGATCC TTTTTGATAA TCTCATGACC AAAATCCCTT AACGTGAGTT
3481 TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT
3541 TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG
3601 TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA
3661 GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT
3721 AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA
3781 TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC
3841 GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT
3901 GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA
3961 CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG
4021 AAACGCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGATT
4081 TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT
4141 ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCCTGCGT TATCCCCTGA
4201 TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC
4261 GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCTGATGC GGTATTTTCT
4321 CCTTACGCAT CTGTGCGGTA TTTCACACCG CATAAATTCC GACACCATCG AATGGTGCAA

FIG. 29 (continued)

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4381  AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT CAATTCAGGG TGGTGAATGT
4441  GAAACCAGTA ACGTTATACG ATGTCGCAGA GTATGCCGGT GTCTCTTATC AGACCGTTTC
4501  CCGCGTGGTG AACCAGGCCA GCCACGTTTC TGCGAAAACG CGGGAAAAAG TGGAAGCGGC
4561  GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCACAA CAACTGGCGG GCAAACAGTC
4621  GTTGCTGATT GGCGTTGCCA CCTCCAGTCT GGCCCTGCAC GCGCCGTCGC AAATTGTCGC
4681  GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG GTGGTGTCGA TGGTAGAACG
4741  AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAATCTT CTCGCGCAAC GCGTCAGTGG
4801  GCTGATCATT AACTATCCGC TGGATGACCA GGATGCCATT GCTGTGGAAG CTGCCTGCAC
4861  TAATGTTCCG GCGTTATTTC TTGATGTCTC TGACCAGACA CCCATCAACA GTATTATTTT
4921  CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCATCTG GTCGCATTGG GTCACCAGCA
4981  AATCGCGCTG TTAGCGGGCC CATTAAGTTC TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG
5041  GCATAAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG
5101  TGCCATGTCC GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACTGC
5161  GATGCTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG CGCGCCATTA CCGAGTCCGG
5221  GCTGCGCGTT GGTGCGGATA TCTCGGTAGT GGGATACGAC GATACCGAAG ACAGCTCATG
5281  TTATATCCCG CCGTTAACCA CCATCAAACA GGATTTTCGC CTGCTGGGGC AAACCAGCGT
5341  GGACCGCTTG CTGCAACTCT CTCAGGGCCA GGCGGTGAAG GGCAATCAGC TGTTGCCCGT
5401  CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG CAAACCGCCT CTCCCCGCGC
5461  GTTGGCCGAT TCATTAATGC AGCTGGCACG ACAGGTTTCC CGACTGGAAA GCGGGCAGTG
5521  AGCGCAACGC AATTAATGTG AGTTAGCTCA CTCATTAGGC ACCCCAGGCT TTACACTTTA
5581  TGCTTCCGGC TCGTATGTTG TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA
5641  GCTATGACCA TGATTACGGA TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC
5701  CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT
5761  AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG
5821  CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT
5881  CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC
5941  ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT
6001  CCGACGGGTT GTTACTCGCT CACATTTAAT GTTGATGAAA GCTGGCTACA GGAAGGCCAG
6061  ACGCGAATTA TTTTTGATGG CGTTGGAATT
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FIG. 29 (continued)

(SEQ ID NO:66) ICT1024 coding region: 310-2879

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   1 TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61 TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121 CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181 GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241 AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301 GGATCCGAAT TCCATGAGTG AGGCCCGCAG GGACAGCACG AGCAGCCTGC AGCGCAAGAA
 361 GCCACCCTGG CTAAAGCTGG ACATTCCCTC TGCGGTGCCC CTGACGGCAG AAGAGCCCAG
 421 CTTCCTGCAG CCCCTGAGGC GACAGGCTTT CCTGAGGAGT GTGAGTATGC CAGCCGAGAC
 481 AGCCCACATC TCTTCACCCC ACCATGAGCT CCGGCGGCCG GTGCTGCAAC GCCAGACGTC
 541 CATCACACAG ACCATCCGCA GGGGGACCGC CGACTGGTTT GGAGTGAGCA AGGACAGTGA
 601 CAGCACCCAG AAATGGCAGC GCAAGAGCAT CCGTCACTGC AGCCAGCGCT ACGGGAAGCT
 661 GAAGCCCCAG GTCCTCCGGG AGCTGGACCT GCCCAGCCAG GACAACGTGT CGCTGACCAG
 721 CACCGAGACG CCACCCCCAC TCTACGTGGG GCCATGCCAG CTGGGCATGC AGAAGATCAT
 781 AGACCCCCTG GCCCGTGGCC GTGCCTTCCG TGTGGCAGAT GACACTGCGG AAGGCCTGAG
 841 TGCCCCACAC ACTCCCGTCA CGCCGGGTGC TGCCTCCCTC TGCTCCTTCT CCAGCTCCCG
 901 CTCAGGTTTC CACCGGCTCC CGCGGCGGCG CAAGCGAGAG TCGGTGGCCA AGATGAGCTT
 961 CCGGGCGGCC GCAGCGCTGA TGAAAGGCCG CTCCGTTAGG GATGGCACCT TTCGCCGGGC
1021 ACGGCGTCGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG ATTTCCCCGA
1081 TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA
1141 CCCGGATGAA GTTTTCGAGT CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC
1201 GGAGCAGGCG GACCTCACCG GCGGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT
1261 GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC
1321 CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCGACGGG GCCAGCGTAT
1381 CGCGGTGCCG GTGCGCAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC TGGGCATGGT
1441 GGGACGGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT
1501 CGAGGACATG GACGACCACA GGCCCTTCTT CACCTACTGG CTTACCTTCG TGCACTCGCT
1561 CGTCACCATC CTAGCCGTGT GCATCTATGG CATCGCGCCC GTGGGCTTCT CGCAGCATGA
1621 GACGGTGGAC TCGGTGCTGC GGAACCGCGG GGTCTACGAG AACGTCAAGT ACGTGCAGCA
1681 GGAGAACTTC TGGATCGGGC CCAGCTCGGA GGCCCTCATC CACCTGGGCG CCAAGTTTTC
1741 GCCCTGCATG CGCCAGGACC CGCAGGTGCA CAGCTTCATT CGCTCGGCGC GCGAGCGCGA
1801 GAAGCACTCC GCCTGCTGCG TGCGCAACGA CAGGTCGGGC TGCGTGCAGA CCTCGGAGGA
1861 GGAGTGCTCG TCCACGCTGG CAGTGTGGGT GAAGTGGCCC ATCCATCCCA GCGCCCCAGA
1921 GCTTGCGGGC CACAAGAGAC AGTTTGGCTC TGTCTGCCAC CAGGATCCCA GGGTGTGTGA
1981 TGAGCCCTCC TCCGAAGACC CTCATGAGTG GCCAGAAGAC ATCACCAAGT GGCCGATCTG
2041 CACCAAAAAC AGCGCTGGGA ACCACACCAA CCATCCCCAC ATGGACTGTG TCATCACAGG
2101 ACGGCCCTGC TGCATTGGCA CCAAGGGCAG GTGTGAGATC ACCTCCCGGG AGTACTGTGA
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FIG. 30

2161 CTTCATGAGG GGCTACTTCC ATGAGGAGGC CACGCTCTGC TCTCAGGTGC ACTGCATGGA
2221 TGATGTGTGT GGGCTCCTGC CTTTTCTCAA CCCCGAGGTG CCTGACCAGT TCTACCGCCT
2281 GTGGCTATCC CTCTTCCTGC ACGCCGGGAT CTTGCACTGC CTGGTGTCCA TCTGCTTCCA
2341 GATGACTGTC CTGCGGGACC TGGAGAAGCT GGCAGGCTGG CACCGCATAG CCATCATCTA
2401 CCTGCTGAGT GGTGTCACCG GCAACCTGGC CAGTGCCATC TTCCTGCCAT ACCGAGCAGA
2461 GGTGGGTCCT GCTGGCTCCC AGTTCGGCAT CCTGGCCTGC CTCTTCGTGG AGCTCTTCCA
2521 GAGCTGGCAG ATCCTGGCGC GGCCCTGGCG TGCCTTCTTC AAGCTGCTGG CTGTGGTGCT
2581 CTTCCTCTTC ACCTTTGGGC TGCTGCCGTG GATTGACAAC TTTGCCCACA TCTCGGGGTT
2641 CATCAGTGGC CTCTTCCTCT CCTTCGCCTT CTTGCCCTAC ATCAGCTTTG GCAAGTTCGA
2701 CCTGTACCGG AAACGCTGCC AGATCATCAT CTTTCAGGTG GTCTTCCTGG GCCTCCTGGC
2761 TGGCCTGGTG GTCCTCTTCT ACGTCTATCC TGTCCGCTGT GAGTGGTGTG AGTTCCTCAC
2821 CTGCATCCCC TTCACTGACA AGTTCTGTGA GAAGTACGAA CTGGACGCTC AGCTCCACAT
2881 CGATACGCGT TCGAAGCTTG CGGCCGCACA GCTGTATACA CGTGCAAGCC AGCCAGAACT
2941 CGCTCCTGAA GACCCAGAGG ATCTCGAGCA CCACCACCAC CACCACTAAT GTTAATTAAG
3001 TTGGGCGTTG TAATCATAGT CATAATCAAT ACTCCTGACT GCGTTAGCAA TTTAACTGTG
3061 ATAAACTACC GCATTAAAGC TATTCGATGA TAAGCTGTCA AACATGATAA TTCTTGAAGA
3121 CGAAAGGGCC TAGGCTGATA AAACAGAATT TGCCTGGCGG CAGTAGCGCG GTGGTCCCAC
3181 CTGACCCCAT GCCGAACTCA GAAGTGAAAC GCCGTAGCGC CGATGGTAGT GTGGGGTCTC
3241 CCCATGCGAG AGTAGGGAAC TGCCAGGCAT CAAATAAAAC GAAAGGCTCA GTCGAAAGAC
3301 TGGGCCTTTC GTTTTATCTG TTGTTTGTCG GTGAACGCTC TCCTGAGTAG GACAAATCCG
3361 CCGGGAGCGG ATTTGAACGT TGCGAAGCAA CGGCCCGGAG GGTGGCGGGC AGGACGCCCG
3421 CCATAAACTG CCAGGCATCA AATTAAGCAG AAGGCCATCC TGACGGATGG CCTTTTTGCG
3481 TTTCTACAAA CTCTTTTGTT TATTTTTCTA AATACATTCA AATATGTATC CGCTGAGCAA
3541 TAACTAGCAT AACCCCTTGG GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA
3601 GGAACTATAT CCGGATTGGC GAATGGGACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG
3661 GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT
3721 TCGCTTTCTT CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC
3781 GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG
3841 ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA
3901 CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTTCCA AACTGGAACA ACACTCAACC
3961 CTATCTCGGT CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA
4021 AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGTTTACAA
4081 TTTCTGGCGG CACGATGGCA TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA
4141 TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA
4201 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT
4261 TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG
4321 TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA

FIG. 30 (continued)

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4381  GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC
4441  TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT
4501  TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG
4561  CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT
4621  TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT
4681  GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT
4741  GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC
4801  TTGCCCGGCG TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT
4861  CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT TGAGATCCAG
4921  TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT
4981  TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG
5041  GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATCATGA CCAAAATCCC TTAACGTGAG
5101  TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT
5161  TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT
5221  TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG
5281  CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT
5341  GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC
5401  GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG
5461  TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
5521  CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG
5581  GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG
5641  GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA
5701  TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT
5761  TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT
5821  GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA
5881  ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCCGGCG ATAATGGCCT GCTTCTCGCC
5941  GAAACGTTTG GTGGCGGGAC CAGTGACGAA GGCTTGAGCG AGGGCGTGCA AGATTCCGAA
6001  TACCGCAAGC GACAGGCCGA TCATCGTCGC GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT
6061  GACCCAGAGC GCTGCCGGCA CCTGTCCTAC GAGTTGCATG ATAAAGAAGA CAGTCATAAG
6121  TGCGGCGACG ACCGGTGAAT TGTGAGCGCT CACAATTCTC GTGACATCAT AACGTCCCGC
6181  GAAAT
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FIG. 30 (continued)

(SEQ ID NO:68) Coding region for the N terminus 400 aa of ICT1024: 314-1515

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   1 TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61 TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121 CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181 GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241 AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301 GGATCCGAAT TCCATGAGTG AGGCCCGCAG GGACAGCACG AGCAGCCTGC AGCGCAAGAA
 361 GCCACCCTGG CTAAAGCTGG ACATTCCCTC TGCGGTGCCC CTGACGGCAG AAGAGCCCAG
 421 CTTCCTGCAG CCCCTGAGGC GACAGGCTTT CCTGAGGAGT GTGAGTATGC CAGCCGAGAC
 481 AGCCCACATC TCTTCACCCC ACCATGAGCT CCGGCGGCCG GTGCTGCAAC GCCAGACGTC
 541 CATCACACAG ACCATCCGCA GGGGGACCGC CGACTGGTTT GGAGTGAGCA AGGACAGTGA
 601 CAGCACCCAG AAATGGCAGC GCAAGAGCAT CCGTCACTGC AGCCAGCGCT ACGGGAAGCT
 661 GAAGCCCCAG GTCCTCCGGG AGCTGGACCT GCCCAGCCAG GACAACGTGT CGCTGACCAG
 721 CACCGAGACG CCACCCCCAC TCTACGTGGG GCCATGCCAG CTGGGCATGC AGAAGATCAT
 781 AGACCCCCTG GCCCGTGGCC GTGCCTTCCG TGTGGCAGAT GACACTGCGG AAGGCCTGAG
 841 TGCCCCACAC ACTCCCGTCA CGCCGGGTGC TGCCTCCCTC TGCTCCTTCT CCAGCTCCCG
 901 CTCAGGTTTC CACCGGCTCC CGCGGCGGCG CAAGCGAGAG TCGGTGGCCA AGATGAGCTT
 961 CCGGGCGGCC GCAGCGCTGA TGAAAGGCCG CTCCGTTAGG GATGGCACCT TTCGCCGGGC
1021 ACGGCGTCGA AGCTTCACTC CAGCTAGCTT TCTGGAGGAG GACACAACTG ATTTCCCCGA
1081 TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA
1141 CCCGGATGAA GTTTTCGAGT CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC
1201 GGAGCAGGCG GACCTCACCG GCGGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT
1261 GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC
1321 CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCGACGGG GCCAGCGTAT
1381 CGCGGTGCCG GTGCGCAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC TGGGCATGGT
1441 GGGACGGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT
1501 CGAGGACATG GACATCGATA CGCGTTCGAA GCTTGCGGCC GCACAGCTGT ATACACGTGC
1561 AAGCCAGCCA GAACTCGCTC CTGAAGACCC AGAGGATCTC GAGCACCACC ACCACCACCA
1621 CTAATGTTAA TTAAGTTGGG CGTTGTAATC ATAGTCATAA TCAATACTCC TGACTGCGTT
1681 AGCAATTTAA CTGTGATAAA CTACCGCATT AAAGCTATTC GATGATAAGC TGTCAAACAT
1741 GATAATTCTT GAAGACGAAA GGGCCTAGGC TGATAAAACA GAATTTGCCT GGCGGCAGTA
1801 GCGCGGTGGT CCCACCTGAC CCCATGCCGA ACTCAGAAGT GAAACGCCGT AGCGCCGATG
1861 GTAGTGTGGG GTCTCCCCAT GCGAGAGTAG GGAACTGCCA GGCATCAAAT AAAACGAAAG
1921 GCTCAGTCGA AAGACTGGGC CTTTCGTTTT ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG
1981 AGTAGGACAA ATCCGCCGGG AGCGGATTTG AACGTTGCGA AGCAACGGCC CGGAGGGTGG
2041 CGGGCAGGAC GCCCGCCATA AACTGCCAGG CATCAAATTA AGCAGAAGGC CATCCTGACG
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FIG. 31

2101 GATGGCCTTT TTGCGTTTCT ACAAACTCTT TTGTTTATTT TTCTAAATAC ATTCAAATAT
2161 GTATCCGCTG AGCAATAACT AGCATAACCC CTTGGGGCCT CTAAACGGGT CTTGAGGGGT
2221 TTTTTGCTGA AAGGAGGAAC TATATCCGGA TTGGCGAATG GGACGCGCCC TGTAGCGGCG
2281 CATTAAGCGC GGCGGGTGTG GTGGTTACGC GCAGCGTGAC CGCTACACTT GCCAGCGCCC
2341 TAGCGCCCGC TCCTTTCGCT TTCTTCCCTT CCTTTCTCGC CACGTTCGCC GGCTTTCCCC
2401 GTCAAGCTCT AAATCGGGGG CTCCCTTTAG GGTTCCGATT TAGTGCTTTA CGGCACCTCG
2461 ACCCCAAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG
2521 TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG TTCCAAACTG
2581 GAACAACACT CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGCCGATTT
2641 CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT TTTAACAAAA
2701 TATTAACGTT TACAATTTCT GGCGGCACGA TGGCATGAGA TTATCAAAAA GGATCTTCAC
2761 CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC
2821 TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT
2881 TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT
2941 ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT
3001 ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC
3061 CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
3121 TAGTTTGCGC AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG
3181 TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT
3241 GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC
3301 AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT
3361 AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG
3421 GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC
3481 TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC
3541 GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT
3601 TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG
3661 AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT CATGACCAAA
3721 ATCCCTTAAC GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAAA GATCAAAGGA
3781 TCTTCTTGAG ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG
3841 CTACCAGCGG TGGTTTGTTT GCCGGATCAA GAGCTACCAA CTCTTTTTCC GAAGGTAACT
3901 GGCTTCAGCA GAGCGCAGAT ACCAAATACT GTCCTTCTAG TGTAGCCGTA GTTAGGCCAC
3961 CACTTCAAGA ACTCTGTAGC ACCGCCTACA TACCTCGCTC TGCTAATCCT GTTACCAGTG
4021 GCTGCTGCCA GTGGCGATAA GTCGTGTCTT ACCGGGTTGG ACTCAAGACG ATAGTTACCG
4081 GATAAGGCGC AGCGGTCGGG CTGAACGGGG GGTTCGTGCA CACAGCCCAG CTTGGAGCGA
4141 ACGACCTACA CCGAACTGAG ATACCTACAG CGTGAGCTAT GAGAAAGCGC CACGCTTCCC
4201 GAAGGGAGAA AGGCGGACAG GTATCCGGTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG
4261 AGGGAGCTTC CAGGGGGAAA CGCCTGGTAT CTTTATAGTC CTGTCGGGTT TCGCCACCTC

FIG. 31 (continued)

```
4321  TGACTTGAGC GTCGATTTTT GTGATGCTCG TCAGGGGGGC GGAGCCTATG GAAAAACGCC
4381  AGCAACGCGG CCTTTTTACG GTTCCTGGCC TTTTGCTGGC CTTTTGCTCA CATGTTCTTT
4441  CCTGCGTTAT CCCCTGATTC TGTGGATAAC CGTATTACCG CCTTTGAGTG AGCTGATACC
4501  GCTCGCCGCA GCCGAACGAC CGAGCGCAGC GAGTCAGTGA GCGAGGAAGC CGGCGATAAT
4561  GGCCTGCTTC TCGCCGAAAC GTTTGGTGGC GGGACCAGTG ACGAAGGCTT GAGCGAGGGC
4621  GTGCAAGATT CCGAATACCG CAAGCGACAG GCCGATCATC GTCGCGCTCC AGCGAAAGCG
4681  GTCCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA
4741  GAAGACAGTC ATAAGTGCGG CGACGACCGG TGAATTGTGA GCGCTCACAA TTCTCGTGAC
4801  ATCATAACGT CCCGCGAAAT
```

FIG. 31 (continued)

(SEQ ID NO 69)Coding region for the C terminus 373 aa of ICT1024: 308-1431

```
   1 TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT
  61 TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG
 121 CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA
 181 GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC
 241 AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGGAGCTCGT
 301 GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG AGAAGCACTC
 361 CGCCTGCTGC GTGCGCAACG ACAGGTCGGG CTGCGTGCAG ACCTCGGAGG AGGAGTGCTC
 421 GTCCACGCTG GCAGTGTGGG TGAAGTGGCC CATCCATCCC AGCGCCCCAG AGCTTGCGGG
 481 CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC AGGGTGTGTG ATGAGCCCTC
 541 CTCCGAAGAC CCTCATGAGT GGCCAGAAGA CATCACCAAG TGGCCGATCT GCACCAAAAA
 601 CAGCGCTGGG AACCACACCA ACCATCCCCA CATGGACTGT GTCATCACAG GACGGCCCTG
 661 CTGCATTGGC ACCAAGGGCA GGTGTGAGAT CACCTCCCGG GAGTACTGTG ACTTCATGAG
 721 GGGCTACTTC CATGAGGAGG CCACGCTCTG CTCTCAGGTG CACTGCATGG ATGATGTGTG
 781 TGGGCTCCTG CCTTTTCTCA ACCCCGAGGT GCCTGACCAG TTCTACCGCC TGTGGCTATC
 841 CCTCTTCCTG CACGCCGGGA TCTTGCACTG CCTGGTGTCC ATCTGCTTCC AGATGACTGT
 901 CCTGCGGGAC CTGGAGAAGC TGGCAGGCTG GCACCGCATA GCCATCATCT ACCTGCTGAG
 961 TGGTGTCACC GGCAACCTGG CCAGTGCCAT CTTCCTGCCA TACCGAGCAG AGGTGGGTCC
1021 TGCTGGCTCC CAGTTCGGCA TCCTGGCCTG CCTCTTCGTG GAGCTCTTCC AGAGCTGGCA
1081 GATCCTGGCG CGGCCCTGGC GTGCCTTCTT CAAGCTGCTG GCTGTGGTGC TCTTCCTCTT
1141 CACCTTTGGG CTGCTGCCGT GGATTGACAA CTTTGCCCAC ATCTCGGGGT TCATCAGTGG
1201 CCTCTTCCTC TCCTTCGCCT TCTTGCCCTA CATCAGCTTT GGCAAGTTCG ACCTGTACCG
1261 GAAACGCTGC CAGATCATCA TCTTTCAGGT GGTCTTCCTG GGCCTCCTGG CTGGCCTGGT
1321 GGTCCTCTTC TACGTCTATC CTGTCCGCTG TGAGTGGTGT GAGTTCCTCA CCTGCATCCC
1381 CTTCACTGAC AAGTTCTGTG AGAAGTACGA ACTGGACGCT CAGCTCCACA TCGATACGCG
1441 TTCGAAGCTT GCGGCCGCAC AGCTGTATAC ACGTGCAAGC CAGCCAGAAC TCGCTCCTGA
1501 AGACCCAGAG GATCTCGAGC ACCACCACCA CCACCACTAA TGTTAATTAA GTTGGGCGTT
1561 GTAATCATAG TCATAATCAA TACTCCTGAC TGCGTTAGCA ATTTAACTGT GATAAACTAC
1621 CGCATTAAAG CTATTCGATG ATAAGCTGTC AAACATGATA ATTCTTGAAG ACGAAAGGGC
1681 CTAGGCTGAT AAAACAGAAT TTGCCTGGCG GCAGTAGCGC GGTGGTCCCA CCTGACCCCA
1741 TGCCGAACTC AGAAGTGAAA CGCCGTAGCG CCGATGGTAG TGTGGGGTCT CCCCATGCGA
1801 GAGTAGGGAA CTGCCAGGCA TCAAATAAAA CGAAAGGCTC AGTCGAAAGA CTGGGCCTTT
1861 CGTTTTATCT GTTGTTTGTC GGTGAACGCT CTCCTGAGTA GGACAAATCC GCCGGGAGCG
1921 GATTTGAACG TTGCGAAGCA ACGGCCCGGA GGGTGGCGGG CAGGACGCCC GCCATAAACT
1981 GCCAGGCATC AAATTAAGCA GAAGGCCATC CTGACGGATG GCCTTTTTGC GTTTCTACAA
2041 ACTCTTTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTGAGCA ATAACTAGCA
```

FIG. 32

2101 TAACCCCTTG GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT TGCTGAAAGG AGGAACTATA
2161 TCCGGATTGG CGAATGGGAC GCGCCCTGTA GCGGCGCATT AAGCGCGGCG GGTGTGGTGG
2221 TTACGCGCAG CGTGACCGCT ACACTTGCCA GCGCCCTAGC GCCCGCTCCT TTCGCTTTCT
2281 TCCCTTCCTT TCTCGCCACG TTCGCCGGCT TTCCCCGTCA AGCTCTAAAT CGGGGGCTCC
2341 CTTTAGGGTT CCGATTTAGT GCTTTACGGC ACCTCGACCC CAAAAAACTT GATTAGGGTG
2401 ATGGTTCACG TAGTGGGCCA TCGCCCTGAT AGACGGTTTT TCGCCCTTTG ACGTTGGAGT
2461 CCACGTTCTT TAATAGTGGA CTCTTGTTCC AAACTGGAAC AACACTCAAC CCTATCTCGG
2521 TCTATTCTTT TGATTTATAA GGGATTTTGC CGATTTCGGC CTATTGGTTA AAAAATGAGC
2581 TGATTTAACA AAAATTTAAC GCGAATTTTA ACAAAATATT AACGTTTACA ATTTCTGGCG
2641 GCACGATGGC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG
2701 AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT
2761 AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG TTGCCTGACT
2821 CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT
2881 GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG
2941 AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG
3001 TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT
3061 TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC
3121 CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT
3181 CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC
3241 AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA
3301 GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGC
3361 GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA
3421 ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA
3481 ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG
3541 AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG
3601 AATACTCATA CTCTTCCTTT TTCAATCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC
3661 CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG
3721 CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG
3781 GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA
3841 AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG
3901 CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG
3961 TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA
4021 ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC
4081 CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT
4141 CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC
4201 TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA
4261 TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC

FIG. 32 (continued)

```
4321  CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG
4381  GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG
4441  CGCAGCGAGT CAGTGAGCGA GGAAGCCGGC GATAATGGCC TGCTTCTCGC CGAAACGTTT
4501  GGTGGCGGGA CCAGTGACGA AGGCTTGAGC GAGGGCGTGC AAGATTCCGA ATACCGCAAG
4561  CGACAGGCCG ATCATCGTCG CGCTCCAGCG AAAGCGGTCC TCGCCGAAAA TGACCCAGAG
4621  CGCTGCCGGC ACCTGTCCTA CGAGTTGCAT GATAAAGAAG ACAGTCATAA GTGCGGCGAC
4681  GACCGGTGAA TTGTGAGCGC TCACAATTCT CGTGACATCA TAACGTCCCG CGAAAT
```

FIG. 32 (continued)

USER PARAMETERS AND SCORING INFORMATION	
METHOD SELECTED TO LIMIT NUMBER OF RESULTS	EXPLICIT NUMBER
NUMBER OF RESULTS REQUESTED	20
HLA MOLECULE TYPE SELECTED	A_0201
LENGTH SELECTED FOR SUBSEQUENCES TO BE SCORED	9
ECHOING MODE SELECTED FOR INPUT SEQUENCE	Y
ECHOING FORMAT	NUMBERED LINES
LENGTH OF USER'S INPUT PEPTIDE SEQUENCE	803
NUMBER OF SUBSEQUENCE SCORES CALCULATED	795
NUMBER OF TOP-SCORING SUBSEQUENCES REPORTED BACK IN SCORING OUTPUT TABLE	20

SCORING RESULTS			
RANK	START POSITION	SUBSEQUENCE RESIDUE LISTING	SCORE (ESTIMATE OF HALF TIME OF DISASSOCIATION OF A MOLECULE CONTAINING THIS SUBSEQUENCE)
1	425	MMPKYLNFV	1080.239
2	410	KLYVRRVFI	642.660
3	557	RLLKKGYEV	257.342
4	203	FLVADKVIV	131.175
5	144	LLHVTDTGV	118.238
6	547	KEAESSPFV	106.738
7	639	RLTESPCAL	87.586
8	381	VTFKSILFV	76.863
9	3	ALWVLGLCC	41.234
10	6	VLGLCCVLL	36.316
11	189	SELIGQFGV	29.023
12	741	RMLRLSLNI	27.879
13	451	LQQHKLLKV	27.573
14	280	YVWSSKTET	24.895
15	259	LELDTIKNL	24.638
16	417	FITDDFHDM	24.478
17	467	KTLDMIKKI	17.695
18	463	KLVRKTLDM	17.388
19	429	YLNFVKGVV	17.053
20	197	VGFYSAFLV	16.564

FIG. 33

SUGGESTED MODELS FOR TRANSMEMBRANE TOPOLOGY FOR ICT1025

---> STRONGLY prefered model: N-terminus inside
2 strong transmembrane helices, total score : 2962
from to length score orientation
1 3 19 (17) 2034 i-o
2 191 212 (22) 928 o-i

---> alternative model
2 strong transmembrane helices, total score : 2607
from to length score orientation
1 3 19 (17) 1929 o-i
2 191 213 (23) 678 i-o

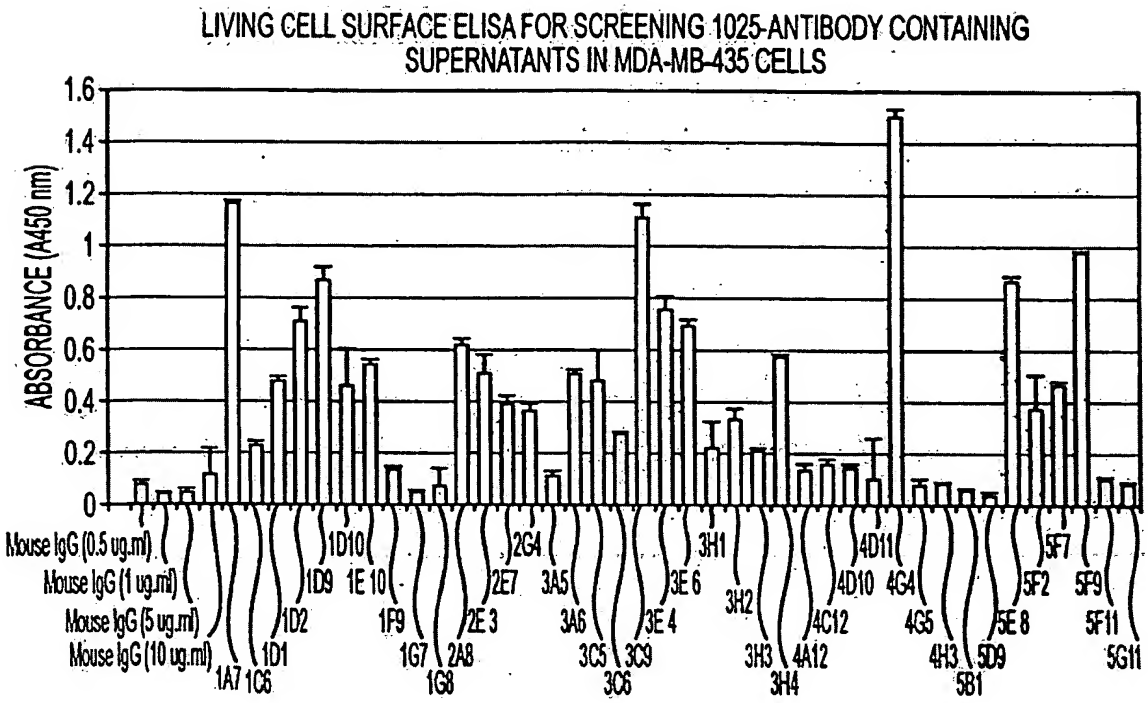
FIG. 34

"DAS" - TRANSMEMBRANE PREDICTION SERVER ICT 1025

POTENTIAL TRANSMEMBRANE SEGMENTS

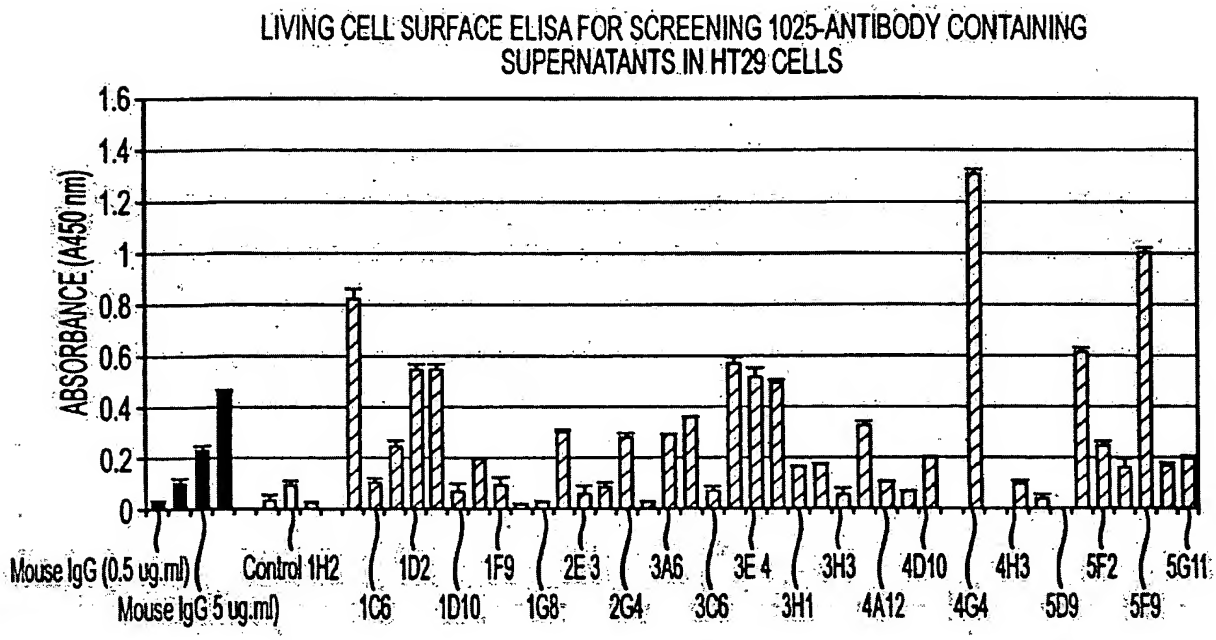
START	STOP	LENGTH		CUTOFF
6	18	13	~	1.7*
7	17	11	~	2.2
195	209	15	~	1.7*
197	206	10	~	2.2
247	248	2	~	1.7
384	390	7	~	1.7
710	723	14	~	1.7
713	719	7	~	2.2*

FIG. 35



SCREENING OF ICT1025 mAb FOR SURFACE BINDING ACTIVITIES IN BREAST TUMOR CELL

FIG. 36



SCREENING OF ICT1025 mAb FOR SURFACE BINDING ACTIVITIES IN COLON TUMOR CELLS

FIG. 37

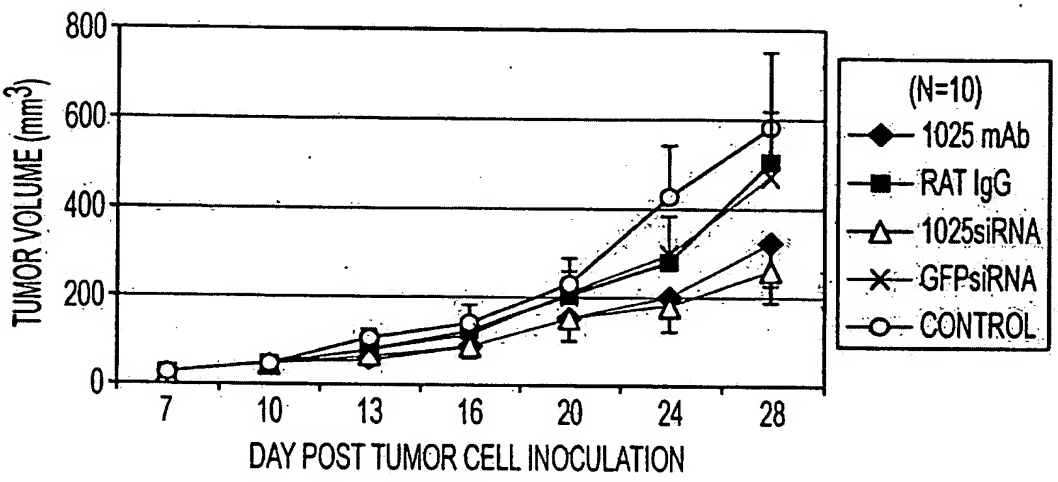

800
600
400
200
0
TUMOR VOLUME (mm3)
7
10
13
16
20
24
28
DAY POST TUMOR CELL INOCULATION
(N=10)
1025 mAb
RAT IgG
1025siRNA
GFPsiRNA
CONTROL

FIG. 38